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GenCore version 4.5

OM protein - protein search, using sw model

Run on: March 6, 2001, 09:42:17 ; Search time 14.27 Seconds
(without alignments)
14.377 Million cell updates/sec

Title: US-09-081-522-4
Perfect score: 33
Sequence: 1 GRGDFV 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 26426

Minimum DB seq length: 0
Maximum DB seq length: 6

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_36:*
1: /SIDS1/gcgdata/geneseq/geneseqp/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqp/AA1981.DAT:*
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21: /SIDS1/gcgdata/geneseq/geneseqp/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	33	100.0	6	16	R82383	Peptide used for t
2	33	100.0	6	16	R82384	Peptide used for t
3	33	100.0	6	16	R82385	Peptide used for t
4	33	100.0	6	16	R82386	Cyclic integrin al
5	33	100.0	6	18	W33056	Alpha-v, beta-5 vi
6	33	100.0	6	19	W41096	Alpha-v beta-3 ant
7	33	100.0	6	19	W41097	Alpha-v beta-3 ant
8	33	100.0	6	19	W41098	Alpha-v beta-3 ant
9	33	100.0	6	19	W41095	Alpha-v beta-3 ant
10	33	100.0	6	19	W41242	Alpha-v-beta-5 ant
11	30	90.9	6	16	R82393	Cyclic integrin al
12	30	90.9	6	19	W41105	Cyclic peptide 621
13	29	87.9	5	12	R11760	Peptide #4 having
14	29	87.9	5	13	R24515	Platelet antagonis
15	29	87.9	6	14	R69327	Gp IIb/IIIa recept
16	29	87.9	6	14	R69331	Gp IIb/IIIa recept
17	29	87.9	6	19	W52091	Targetting peptide
18	29	87.9	6	19	W52094	Targetting peptide
19	29	87.9	6	19	W50596	GPIIb/IIIa recepto
20	29	87.9	6	21	Y54947	Peptide ligand for
21	29	87.9	6	21	Y54951	Peptide ligand for
22	27	81.8	5	15	R45382	Cell adhesion inhi
23	27	81.8	5	15	R45384	Cell adhesion inhi
24	27	81.8	5	15	R45386	Cell adhesion inhi
25	27	81.8	5	15	R45387	Cell adhesion inhi
26	27	81.8	5	16	R82387	Cyclic integrin al
27	27	81.8	5	16	R82389	Cyclic integrin al
28	27	81.8	5	18	W33057	Alpha-v, beta-5 vi
29	27	81.8	5	18	W33055	Alpha-v, beta-5 vi
30	27	81.8	5	19	W41099	Alpha-v beta-3 ant
31	27	81.8	5	19	W41101	Alpha-v beta-3 ant
32	27	81.8	5	19	W41109	Alpha-v beta-3 ant
33	27	81.8	5	19	W41240	Alpha-v-beta-5 ant
34	27	81.8	5	19	W41243	Alpha-v-beta-5 ant
35	27	81.8	5	19	W41247	Alpha-v-beta-5 ant
36	27	81.8	5	20	W92307	Cyclic azapeptide
37	27	81.8	6	15	R45370	Cell adhesion inhi
38	27	81.8	6	15	R45372	Cell adhesion inhi
39	27	81.8	6	15	R45374	Cell adhesion inhi
40	27	81.8	6	15	R45376	Cell adhesion inhi
41	27	81.8	6	15	R45377	Cell adhesion inhi
42	27	81.8	6	18	Y08057	Biotin derivative
43	26	78.8	5	12	R11757	Peptide #1 having
44	26	78.8	5	13	R24518	Platelet antagonis
45	26	78.8	5	15	R63576	Covalently binding

ALIGNMENTS

RESULT 1
R82383
ID R82383 standard; peptide; 6 AA.
XX
AC R82383;
XX
DT 03-MAY-1996 (first entry)
XX
DE Peptide used for the synthesis of integrin alpha-v-beta-3 inhibitors.
XX
KW Integrin; alpha-v-beta-3; inhibitor; angiogenesis; antagonist;
KW fibrinogen; inflammation; apoptosis; restenosis.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "BOC-Gly, the N-terminal is protected by a
FT butyloxycarbonyl group"
FT Misc-difference 2
FT /note= "D-Arg"
FT Modified-site 6
FT /note= "Val-OMe, the C-terminal is protected by
FT a methyl ester group"
XX
PN WO9525543-A1.
XX
PD 28-SEP-1995.
XX
PF 09-MAR-1995; 95WO-US03035.
XX
PR 30-DEC-1994; 94US-0366665.
PR 18-MAR-1994; 94US-0210715.
XX
PA (SCRI) SCRIPPS RES INST.

```
XX
PI   Brooks P,  Cheresh DA;
XX
DR   WPI; 1995-344463/44.
XX
PT   Inhibition of angiogenesis in a tissue, e.g. following angioplasty
PT   - by admin. of a compsn. comprising an alpha-v-beta3 antagonist,
PT   useful for regression of established tumours, treating inflamed
PT   tissue, etc.
XX
PS   Example 1; Page 95; 135pp; English.
XX
CC   The peptides R82383-85 are peptides used in the synthesis of a group
CC   of inhibitor peptides of integrin alpha-v-beta-3. The inhibitor
CC   peptides (R82386-96) may be  administered in a compsn. and are useful
CC   for inhibition of inflamed tissue angiogenesis, e.g. that associated
CC   with rheumatoid arthritis, retinal angiogenesis associated with
CC   diabetic retinopathy, that associated with haemangioma, solid
CC   tumours, or solid tumour metastases. The alpha-v-beta-3 antagonists
CC   are also useful to induce apoptosis in neovasculature in a tissue.
CC   The inhibitor peptides are pref. cyclic and contain an RGD sequence.
XX
SQ   Sequence   6 AA;


  Query Match             100.0%;  Score 33;  DB 16;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GRGDFV 6
          ||||||
Db      1 grgdfv 6


RESULT  2
R82384
ID   R82384 standard; peptide; 6 AA.
XX
AC   R82384;
XX
DT   03-MAY-1996  (first entry)
XX
DE   Peptide used for the synthesis of integrin alpha-v-beta-3 inhibitors.
XX
KW   Integrin; alpha-v-beta-3; inhibitor; angiogenesis; antagonist;
KW   fibrinogen; inflammation; apoptosis; restenosis.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1
FT                   /note= "BOC-Gly, the N-terminal is protected by a
FT                         butyloxycarbonyl group"
FT   Misc-difference 2
FT                   /note= "D-Arg"
XX
PN   WO9525543-A1.
XX
PD   28-SEP-1995.
XX
PF   09-MAR-1995;   95WO-US03035.
XX
PR   30-DEC-1994;   94US-0366665.
PR   18-MAR-1994;   94US-0210715.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Brooks P,  Cheresh DA;
XX
DR   WPI; 1995-344463/44.
XX
PT   Inhibition of angiogenesis in a tissue, e.g. following angioplasty
PT   - by admin. of a compsn. comprising an alpha-v-beta3 antagonist,
PT   useful for regression of established tumours, treating inflamed
PT   tissue, etc.
XX
PS   Example 1; Page 96; 135pp; English.
XX
CC   The peptides R82383-85 are peptides used in the synthesis of a group
CC   of inhibitor peptides of integrin alpha-v-beta-3. The inhibitor
CC   peptides (R82386-96) may be  administered in a compsn. and are useful
CC   for inhibition of inflamed tissue angiogenesis, e.g. that associated
CC   with rheumatoid arthritis, retinal angiogenesis associated with
CC   diabetic retinopathy, that asscoiated with haemangioma, solid
CC   tumours, or solid tumour metastases. The alpha-v-beta-3 atagonists
CC   are also useful to induce apoptosis in neovasculature in a tissue.
CC   The inhibitor peptides are pref. cyclic and contain an RGD sequence.
XX
SQ   Sequence   6 AA;


  Query Match             100.0%;  Score 33;  DB 16;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GRGDFV 6
          ||||||
Db      1 grgdfv 6


RESULT  3
R82385
ID   R82385 standard; peptide; 6 AA.
XX
AC   R82385;
XX
DT   03-MAY-1996  (first entry)
XX
DE   Peptide used for the synthesis of integrin alpha-v-beta-3 inhibitors.
XX
KW   Integrin; alpha-v-beta-3; inhibitor; angiogenesis; antagonist;
KW   fibrinogen; inflammation; apoptosis; restenosis.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 2
FT                   /note= "D-Arg"
XX
PN   WO9525543-A1.
XX
PD   28-SEP-1995.
XX
PF   09-MAR-1995;   95WO-US03035.
XX
PR   30-DEC-1994;   94US-0366665.
PR   18-MAR-1994;   94US-0210715.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Brooks P,  Cheresh DA;
XX
DR   WPI; 1995-344463/44.
XX
PT   Inhibition of angiogenesis in a tissue, e.g. following angioplasty
PT   - by admin. of a compsn. comprising an alpha-v-beta3 antagonist,
PT   useful for regression of established tumours, treating inflamed
PT   tissue, etc.
XX
PS   Example 1; Page 97; 135pp; English.
XX
CC   The peptides R82383-85 are peptides used in the synthesis of a group
CC   of inhibitor peptides of integrin alpha-v-beta-3. The inhibitor
CC   peptides (R82386-96) may be  administered in a compsn. and are useful
CC   for inhibition of inflamed tissue angiogenesis, e.g. that associated
CC   with rheumatoid arthritis, retinal angiogenesis associated with
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CC   diabetic retinopathy, that asscoiated with haemangioma, solid
CC   tumours, or solid tumour metastases. The alpha-v-beta-3 atagonists
CC   are also useful to induce apoptosis in neovasculature in a tissue.
CC   The inhibitor peptides are pref. cyclic and contain an RGD sequence.
XX
SQ   Sequence   6 AA;


  Query Match            100.0%;  Score 33;  DB 16;  Length 6;
  Best Local Similarity  100.0%;  Pred. No. 2.1e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GRGDFV 6
          ||||||
Db      1 grgdfv 6


RESULT   4
R82386
ID   R82386 standard; peptide; 6 AA.
XX
AC   R82386;
XX
DT   03-MAY-1996  (first entry)
XX
DE   Cyclic integrin alpha-v-beta-3 inhibitor peptide no. 62181.
XX
KW   Integrin; alpha-v-beta-3; inhibitor; angiogenesis; antagonist;
KW   fibrinogen; inflammation; apoptosis; restenosis; cyclic.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 2
FT                   /note= "D-Arg"
XX
PN   WO9525543-A1.
XX
PD   28-SEP-1995.
XX
PF   09-MAR-1995;   95WO-US03035.
XX
PR   30-DEC-1994;   94US-0366665.
PR   18-MAR-1994;   94US-0210715.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Brooks P,  Cheresh DA;
XX
DR   WPI; 1995-344463/44.
XX
PT   Inhibition of angiogenesis in a tissue, e.g. following angioplasty
PT   - by admin. of a compsn. comprising an alpha-v-beta3 antagonist,
PT   useful for regression of established tumours, treating inflamed
PT   tissue, etc.
XX
PS   Claim 4; Page 97; 135pp; English.
XX
CC   R82386-96 are a group of inhibitor peptides of integrin alpha-v-beta-3.
CC   The inhibitor peptides may be  administered in a compsn. and are useful
CC   for inhibition of inflamed tissue angiogenesis, e.g. that associated
CC   with rheumatoid arthritis, retinal angiogenesis associated with
CC   diabetic retinopathy, that associated with haemangioma, solid
CC   tumours, or solid tumour metastases. The alpha-v-beta-3 antagonists
CC   are also useful to induce apoptosis in neovasculature in a tissue.
CC   The inhibitor peptides are pref. cyclic and contain an RGD sequence.
XX
SQ   Sequence   6 AA;


  Query Match            100.0%;  Score 33;  DB 16;  Length 6;
  Best Local Similarity  100.0%;  Pred. No. 2.1e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GRGDFV 6
          ||||||
Db      1 grgdfv 6


RESULT   5
W33056
ID   W33056 standard; peptide; 6 AA.
XX
AC   W33056;
XX
DT   26-JAN-1998  (first entry)
XX
DE   Alpha-v, beta-5 vitronectin receptor antagonist.
XX
KW   RGD containing peptide; antagonist; alpha-v, beta-5;
KW   vitronectin receptor; inhibition; angiogenesis; inflammation;
KW   rheumatoid arthritis; eye disease; diabetic retinopathy;
KW   age related macular degeneration; ocular histoplasmosis;
KW   retinopathy; prematurity; neovascular glaucoma;
KW   corneal neovascular disorder; transplantation; herpetic; luetic;
KW   keratitis; pterygium; neovascular pannus; haemangioma;
KW   solid tumour; metastasis; cytokine; low toxicity;
KW   vascular endothelial growth factor;
KW   transforming growth factor alpha; epidermal growth factor; cyclic.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1
FT                   /note= "D-form residue"
XX
PN   WO9706791-A1.
XX
PD   27-FEB-1997.
XX
PF   13-AUG-1996;   96WO-US13194.
XX
PR   14-AUG-1995;   95US-0514799.
PR   14-AUG-1996;   96ZA-0006886.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Brooks P,  Cheresh DA,  Friedlander M;
XX
DR   WPI; 1997-165019/15.
XX
PT   Inhibiting angiogenesis with an antagonist selective for the
PT   alpha-v,beta-5 integrin receptor - e.g. antibody, RGD peptide or
PT   organic mimetic, for treatment of inflammation, eye disease, tumours
PT   etc.
XX
PS   Claim 5; Page 105; 126pp; English.
XX
CC   The present RGD containing peptide is an antagonist of the alpha-v,
CC   beta-5 vitronectin receptor, which can be used to inhibit
CC   angiogenesis in alpha-v, beta-5 containing tissue, specifically
CC   angiogenesis as a result of inflammation (especially rheumatoid
CC   arthritis), eye disease (especially diabetic retinopathy, age
CC   related macular degeneration, ocular histoplasmosis, retinopathy of
CC   prematurity or neovascular glaucoma), corneal neovascular disorders
CC   (especially transplantation, herpetic or luetic keratitis,
CC   pterygium and neovascular pannus associated with wearing contact
CC   lenses), haemangioma, solid tumours and their metastases or
CC   cytokines (especially vascular endothelial growth factor,
CC   transforming growth factor alpha or epidermal growth factor). The
CC   antagonist has the advantage of being very specific, affecting no
CC   processes other than angiogenesis and therefore of relatively low
CC   toxicity.
XX
SQ   Sequence   6 AA;
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Query Match 100.0%; Score 33; DB 18; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRGDFV 6
||||||
Db 1 grgdfv 6

RESULT 6
W41096
ID W41096 standard; Peptide; 6 AA.
XX
AC W41096;
XX
DT 08-JUN-1998 (first entry)
XX
DE Alpha-v beta-3 antagonist precursor peptide.
XX
KW Angiogenesis; inhibitor; antagonist; integrin alpha-v beta-3;
KW vitronectin receptor; rheumatoid arthritis; tumour; metastasis;
KW diabetic retinopathy; macular degeneration; restenosis; therapy.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "N-terminus protected by Boc"
FT Misc-difference 2
FT /note= "D-form residue"
XX
PN WO9745137-A1.
XX
PD 04-DEC-1997.
XX
PF 30-MAY-1997; 97WO-US09158.
XX
PR 31-MAY-1996; 96US-0018733.
PR 31-MAY-1996; 96US-0015869.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Brooks P, Cheresh DA;
XX
DR WPI; 1998-032334/03.
XX
PT Packaging material containing polypeptide antagonist of alphav,
PT beta3 integrin - used for inhibition of angiogenesis, and for
PT treating tumours, inflammation, eye diseases etc.
XX
PS Example 1; Page 47; 234pp; English.
XX
CC This synthetic RGD peptide was used in the preparation of a cyclic
CC peptide, designated 62181 (see W41098), that is an antagonist of
CC integrin alpha-v beta-3. An N- and C-terminally protected peptide
CC (see W41095) was dissolved in methanol to which 2 N NaOH solution
CC was added. The admixture was stirred for 3 hr at 20 degC. After
CC evaporation, the residue was taken up in water, acidified to pH 3
CC with diluted HCl and extracted with ethyl acetate. The peptide
CC product (see W41096), which has a free C-terminal carboxylic acid,
CC was stirred at 20 degC for 2 hr with 2 N HCl in dioxane to obtain a
CC further peptide (see W41097). This was treated with
CC dicyclohexylcarbodiimide, 1-hydroxybenzotriazole and
CC N-methylmorpholine to produce the cyclic peptide. The invention
CC relates to the discovery that angiogenesis is mediated by the
CC specific vitronectin receptor alpha-v beta-3, and that inhibition
CC of alpha-v beta-3 function inhibits angiogenesis. Claimed
CC antagonists of alpha-v beta-3 comprise C-terminal fragments (see
CC W41083-94) of human or chicken matrix metalloproteinase, fusion
CC polypeptides, cyclic or linear polypeptides, derivatised
CC polypeptides, a monoclonal antibody or organic mimetic compound.
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 33; DB 19; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRGDFV 6
||||||
Db 1 grgdfv 6

RESULT 7
W41097
ID W41097 standard; Peptide; 6 AA.
XX
AC W41097;
XX
DT 08-JUN-1998 (first entry)
XX
DE Alpha-v beta-3 antagonist precursor peptide.
XX
KW angiogenesis; inhibitor; antagonist; integrin alpha-v beta-3;
KW vitronectin receptor; rheumatoid arthritis; tumour; metastasis;
KW diabetic retinopathy; macular degeneration; restenosis; therapy.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 2
FT /note= "D-form residue"
XX
PN WO9745137-A1.
XX
PD 04-DEC-1997.
XX
PF 30-MAY-1997; 97WO-US09158.
XX
PR 31-MAY-1996; 96US-0018733.
PR 31-MAY-1996; 96US-0015869.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Brooks P, Cheresh DA;
XX
DR WPI; 1998-032334/03.
XX
PT Packaging material containing polypeptide antagonist of alphav,
PT beta3 integrin - used for inhibition of angiogenesis, and for
PT treating tumours, inflammation, eye diseases etc.
XX
PS Example 1; Page 47; 234pp; English.
XX
CC This synthetic RGD peptide was used in the preparation of a cyclic
CC peptide, designated 62181 (see W41098), that is an antagonist of
CC integrin alpha-v beta-3. An N- and C-terminally protected
CC peptide (see W41095) was dissolved in methanol to which 2
CC N NaOH solution was added. The admixture was stirred for 3 hr at
CC 20 degC. After evaporation, the residue was taken up in water,
CC acidified to pH 3 with diluted HCl and extracted with ethyl acetate.
CC The peptide product (see W41096), which has a free C-terminal
CC carboxylic acid, was stirred at 20 degC for 2 hr with 2 N HCl in
CC dioxane to obtain a further peptide (see W41097), which has free
CC N- and C-terminals. This was treated with dicyclohexylcarbodiimide,
CC 1-hydroxybenzotriazole and N-methylmorpholine to produce the cyclic
CC peptide. The invention relates to the discovery that angiogenesis
CC is mediated by the specific vitronectin receptor alpha-v beta-3,
CC and that inhibition of alpha-v beta-3 function inhibits angiogenesis.
CC Claimed antagonists of alpha-v beta-3 comprise C-terminal fragments
CC (see W41083-94) of human or chicken matrix metalloproteinase-2,
CC fusion polypeptides, cyclic or linear polypeptides, derivatised
CC polypeptides, a monoclonal antibody or organic mimetic compound.
XX

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SQ   Sequence   6 AA;

  Query Match             100.0%;  Score 33;  DB 19;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GRGDFV 6
          ||||||
Db      1 grgdfv 6


RESULT   8
W41098
ID   W41098 standard; Peptide; 6 AA.
XX
AC   W41098;
XX
DT   08-JUN-1998  (first entry)
XX
DE   Alpha-v beta-3 antagonist cyclic peptide 62181.
XX
KW   Angiogenesis; inhibitor; antagonist; integrin alpha-v beta-3;
KW   vitronectin receptor; rheumatoid arthritis; tumour; metastasis;
KW   diabetic retinopathy; macular degeneration; restenosis; therapy;
KW   circular; cyclic.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 2
FT                   /note= "D-form residue"
XX
PN   WO9745137-A1.
XX
PD   04-DEC-1997.
XX
PF   30-MAY-1997;   97WO-US09158.
XX
PR   31-MAY-1996;   96US-0018733.
PR   31-MAY-1996;   96US-0015869.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Brooks P,  Cheresh DA;
XX
DR   WPI; 1998-032334/03.
XX
PT   Packaging material containing polypeptide antagonist of alphav,
PT   beta3 integrin - used for inhibition of angiogenesis, and for
PT   treating tumours, inflammation, eye diseases etc.
XX
PS   Example 1; Page 48; 234pp; English.
XX
CC   This synthetic RGD-containing cyclic peptide, designated 62181, is
CC   a particularly preferred peptide that has integrin alpha-v beta-3
CC   antagonist activity.  It exhibits preferential inhibition of
CC   fibrinogen binding to the alpha v beta-3 receptor.  It can be
CC   prepared using standard solid-phase synthesis techniques (see
CC   W41095-97).  The invention relates to the discovery that
CC   angiogenesis is mediated by the specific vitronectin receptor
CC   alpha-v beta-3, and that inhibition of alpha-v beta-3 function
CC   inhibits angiogenesis.  Claimed antagonists of alpha-v beta-3
CC   comprise C-terminal fragments (see W41083-94) of human or chicken
CC   matrix metalloproteinase-2, fusion polypeptides, cyclic or linear
CC   polypeptides, derivatised polypeptides, a monoclonal antibody or
CC   organic mimetic compound.  They can be used to inhibit angiogenesis
CC   in inflammed tissue (for treatment of arthritis or rheumatoid
CC   arthritis), in solid tumours or metastases (particularly to induce
CC   regression or inhibit tumour growth), and in ocular disorders such
CC   as diabetic retinopathy and macular degeneration, as well as to
CC   treat restenosis (all claimed).
XX
```

```
SQ   Sequence   6 AA;

  Query Match             100.0%;  Score 33;  DB 19;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GRGDFV 6
          ||||||
Db      1 grgdfv 6


RESULT   9
W41095
ID   W41095 standard; Peptide; 6 AA.
XX
AC   W41095;
XX
DT   08-JUN-1998  (first entry)
XX
DE   Alpha-v beta-3 antagonist precursor peptide.
XX
KW   Angiogenesis; inhibitor; antagonist; integrin alpha-v beta-3;
KW   vitronectin receptor; rheumatoid arthritis; tumour; metastasis;
KW   diabetic retinopathy; macular degeneration; restenosis; therapy.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1
FT                   /note= "N-terminus protected by Boc"
FT   Misc-difference 2
FT                   /note= "D-form residue"
FT   Modified-site   6
FT                   /note= "C-terminus protected by methyl ester"
XX
PN   WO9745137-A1.
XX
PD   04-DEC-1997.
XX
PF   30-MAY-1997;   97WO-US09158.
XX
PR   31-MAY-1996;   96US-0018733.
PR   31-MAY-1996;   96US-0015869.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Brooks P,  Cheresh DA;
XX
DR   WPI; 1998-032334/03.
XX
PT   Packaging material containing polypeptide antagonist of alphav,
PT   beta3 integrin - used for inhibition of angiogenesis, and for
PT   treating tumours, inflammation, eye diseases etc.
XX
PS   Example 1; Page 47; 234pp; English.
XX
CC   This synthetic RGD peptide was used in the preparation of a cyclic
CC   peptide, designated 62181 (see W41098), that is an antagonist of
CC   integrin alpha-v beta-3.  The peptide was dissolved in methanol to
CC   which 2 N NaOH solution was added.  The admixture was stirred for 3
CC   hr at 20 degC.  After evaporation, the residue was taken up in
CC   water, acidified to pH 3 with diluted HCl and extracted with ethyl
CC   acetate.  The peptide product (see W41096) was stirred at 20 degC
CC   for 2 hr with 2 N HCl in dioxane to obtain a further peptide (see
CC   W41097).  This was treated with dicyclohexylcarbodiimide,
CC   1-hydroxybenzotriazole and N-methylmorpholine to produce peptide
CC   62181.  The invention relates to the discovery that angiogenesis is
CC   mediated by the specific vitronectin receptor alpha-v beta-3, and
CC   that inhibition of alpha-v beta-3 function inhibits angiogenesis.
CC   Claimed antagonists of alpha-v beta-3 comprise C-terminal fragments
CC   (see W41083-94) of human or chicken matrix metalloproteinase-2,
CC   fusion polypeptides, cyclic or linear polypeptides, derivatised
```

```
CC   polypeptides, a monoclonal antibody or organic mimetic compound.
XX
SQ   Sequence   6 AA;


  Query Match            100.0%;  Score 33;  DB 19;  Length 6;
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Qy      1 GRGDFV 6
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Db      1 grgdfv 6


RESULT  10
W41242
ID   W41242 standard; protein; 6 AA.
XX
AC   W41242;
XX
DT   09-JUN-1998  (first entry)
XX
DE   Alpha-v-beta-5 antagonistic peptide 62181.
XX
KW   Alpha-v-beta-5 antagonist; treatment; vitronectin receptor; inhibition;
KW   angiogenesis; tumour growth; restenosis; neovascularisation.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1..6
FT                   /note= "peptide is made cyclic via the first and
FT                         last residues"
FT   Misc-difference 2
FT                   /note= "D-form residue"
XX
PN   WO9745447-A1.
XX
PD   04-DEC-1997.
XX
PF   30-MAY-1997;   97WO-US09099.
XX
PR   31-MAY-1996;   96US-0018733.
PR   31-MAY-1996;   96US-0015859.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Brooks P,  Cheresh DA,  Friedlander M;
XX
DR   WPI; 1998-041758/04.
XX
PT   Packaging material containing polypeptide antagonist of alphav,
PT   beta5 integrin - used for inhibition of angiogenesis, and for
PT   treating tumours, inflammation, eye diseases etc.
XX
PS   Disclosure; Page 41; 117pp; English.
XX
CC   The present peptide represents an alpha-v-beta-5 integrin antagonists.
CC   Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of alpha-v-beta-5
CC   can inhibit angiogenesis. The specification describes a novel
CC   labelled package that contains an inhibitor of angiogenesis i.e. an
CC   alpha-v-beta-5 antagonising polypeptide that binds to integrin
CC   alpha-v-beta-5 and includes a part of the C-terminal domain of MMP-2.
CC   The antagonists are used to inhibit angiogenesis in inflamed tissue, in
CC   solid tumours or metastases, and in a wide range of ocular disorders
CC   (e.g. diabetic or other forms of retinopathy, neovascular glaucoma, or
CC   corneal transplants). They are particularly used to induce regression or
CC   to inhibit growth of tumours. The alpha-v-beta-5 antagonists can also be
CC   used to treat restenosis caused by migration of smooth muscle cells
CC   following angioplasty and to reduce blood supply to selected tissues.
CC   The antagonists particularly inhibit neovascularisation where this is
CC   induced by cytokines, e.g. transforming growth factor alpha, epidermal
CC   growth factor or especially vascular endothelial growth factor.
CC   note: this sequence does not appear in the specification; it was created
CC   using information provided.
XX
SQ   Sequence   6 AA;


  Query Match            100.0%;  Score 33;  DB 19;  Length 6;
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Qy      1 GRGDFV 6
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Db      1 grgdfv 6


RESULT  11
R82393
ID   R82393 standard; peptide; 6 AA.
XX
AC   R82393;
XX
DT   03-MAY-1996  (first entry)
XX
DE   Cyclic integrin alpha-v-beta-3 inhibitor peptide no. 62179.
XX
KW   Integrin; alpha-v-beta-3; inhibitor; angiogenesis; antagonist;
KW   fibrinogen; inflammation; apoptosis; restenosis; cyclic.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 2
FT                   /note= "D-Ala"
XX
PN   WO9525543-A1.
XX
PD   28-SEP-1995.
XX
PF   09-MAR-1995;   95WO-US03035.
XX
PR   30-DEC-1994;   94US-0366665.
PR   18-MAR-1994;   94US-0210715.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Brooks P,  Cheresh DA;
XX
DR   WPI; 1995-344463/44.
XX
PT   Inhibition of angiogenesis in a tissue, e.g. following angioplasty
PT   - by admin. of a compsn. comprising an alpha-v-beta3 antagonist,
PT   useful for regression of established tumours, treating inflamed
PT   tissue, etc.
XX
PS   Example 1; Page 47; 135pp; English.
XX
CC   R82386-96 are a group of inhibitor peptides of integrin alpha-v-beta-3.
CC   The inhibitor peptides may be  administered in a compsn. and are useful
CC   for inhibition of inflamed tissue angiogenesis, e.g. that associated
CC   with rheumatoid arthritis, retinal angiogenesis associated with
CC   diabetic retinopathy, that associated with haemangioma, solid
CC   tumours, or solid tumour metastases. The alpha-v-beta-3 atagonists
CC   are also useful to induce apoptosis in neovasculature in a tissue.
CC   The inhibitor peptides are pref. cyclic and contain an RGD sequence.
XX
SQ   Sequence   6 AA;


  Query Match             90.9%;  Score 30;  DB 16;  Length 6;
  Best Local Similarity   83.3%;  Pred. No. 2.1e+05;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GRGDFV 6
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          |||||:
Db        1 grgdfl 6


RESULT  12
W41105
ID   W41105 standard; Peptide; 6 AA.
XX
AC   W41105;
XX
DT   08-JUN-1998  (first entry)
XX
DE   Cyclic peptide 62179.
XX
KW   Angiogenesis; inhibitor; antagonist; integrin alpha-v beta-3;
KW   vitronectin receptor; rheumatoid arthritis; tumour; metastasis;
KW   diabetic retinopathy; macular degeneration; restenosis; therapy;
KW   circular; cyclic.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 5
FT                   /note= "D-form residue"
XX
PN   WO9745137-A1.
XX
PD   04-DEC-1997.
XX
PF   30-MAY-1997;   97WO-US09158.
XX
PR   31-MAY-1996;   96US-0013733.
PR   31-MAY-1996;   96US-0013869.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Brooks P,  Cheresh DA;
XX
DR   WPI; 1998-032334/03.
XX
PT   Packaging material containing polypeptide antagonist of alphav,
PT   beta3 integrin - used for inhibition of angiogenesis, and for
PT   treating tumours, inflammation, eye diseases etc.
XX
PS   Example 1; Page 51; 234pp; English.
XX
CC   This synthetic cyclic peptide, designated 62179, was examined as
CC   a potential antagonist of integrin alpha-v beta-3.  It was
CC   prepared using standard solid-phase synthesis techniques.  Unlike
CC   RGD-containing or RGD-derivatised cyclic peptides (see W41098-101),
CC   peptide 62179 did not exhibit preferential inhibition of fibrinogen
CC   binding to the alpha-v beta-3 receptor.  The invention relates to
CC   the discovery that angiogenesis is mediated by the specific
CC   vitronectin receptor alpha-v beta-3, and that inhibition of alpha-v
CC   beta-3 function inhibits angiogenesis.  Claimed antagonists of
CC   alpha-v beta-3 comprise C-terminal fragments (see W41083-94) of
CC   human or chicken matrix metalloproteinase-2, fusion polypeptides,
CC   cyclic or linear polypeptides, derivatised polypeptides, a
CC   monoclonal antibody or organic mimetic compound.
XX
SQ   Sequence   6 AA;


  Query Match             90.9%;  Score 30;  DB 19;  Length 6;
  Best Local Similarity   83.3%;  Pred. No. 2.1e+05;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 GRGDFV 6
            |||||:
Db        1 grgdfl 6


RESULT  13
R11760
ID   R11760 standard; Protein; 5 AA.
XX
AC   R11760;
XX
DT   03-JUL-1991  (first entry)
XX
DE   Peptide #4 having cell recognition sequence.
XX
KW   Cell surface adhesion; receptor mediated attachment; culture;
KW   substrate.
XX
OS   Synthetic.
XX
PN   WO9105036-A.
XX
PD   18-APR-1991.
XX
PF   27-SEP-1990;   90WO-US05525.
XX
PR   28-SEP-1989;   89US-0414144.
PR   21-MAY-1990;   90US-0527198.
XX
PA   (TEXA ) UNIV OF TEXAS SYST.
XX
PI   Hubbell JA,  Massia SP,  Desai NP;
XX
DR   WPI; 1991-132844/18.
XX
PT   Surfaces having cell adhesive effects - formed by covalently linking
PT   small peptides which facilitate cell receptor mediated attachment of
PT   cells.
XX
PS   Claim 3; Page 91; 127pp; English.
XX
CC   The peptide, and shorter versions eg RGDF, including the cell
CC   recognition sequence RGDF, can be used to prepare a cell culture
CC   substrate. A surface (glass, PET etc) is chemically derivatised
CC   with the peptides to yield a proteolytically stable, reusable
CC   surface which promotes the amt. of and enhances the rate of receptor
CC   mediated cell adhesion. See also R11757-R11762.
XX
SQ   Sequence   5 AA;


  Query Match             87.9%;  Score 29;  DB 12;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 GRGDF 5
            |||||
Db        1 grgdf 5


RESULT  14
R24515
ID   R24515 standard; Protein; 5 AA.
XX
AC   R24515;
XX
DT   02-DEC-1992  (first entry)
XX
DE   Platelet antagonist pepetide 2.
XX
KW   Clinical effect; antagonist.
XX
OS   Synthetic.
XX
PN   JP04134096-A.
XX
PD   07-MAY-1992.
XX
PF   21-SEP-1990;   90JP-0253849.
```

XX
PR 21-SEP-1990; 90JP-0253849.
XX
PA (SEGK) SEIKAGAKU KOGYO CO LTD.
XX
DR WPI; 1992-204525/25.
XX
PT New peptide(s) comprising arginine-glycine-asparagine and
PT hyaluronic acid - useful as platelet antagonists with higher
PT activity than arginine-glycine-asparagine-valine
XX
PS Disclosure; Page 5; 10pp; Japanese.
XX
CC The sequences given in R24514-8 are peptides which are useful as
CC platelet antagonists. These peptides have higher activity than the
CC conventional peptide of Arg-Gly-Asp-Val. These peptides have a
CC clinical effect at a lower dose, dosage is 2.5-5.0 mg/kg/day.
XX
SQ Sequence 5 AA;

Query Match 87.9%; Score 29; DB 13; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRGDF 5
|||||
Db 1 grgdf 5

RESULT 15
R69327
ID R69327 standard; peptide; 6 AA.
XX
AC R69327;
XX
DT 25-JUN-1995 (first entry)
XX
DE Gp IIb/IIIa receptor ligand used in scintigraphic imaging of thrombi.
XX
KW Scintigraphy; thrombus; thrombi; imaging; specific binding;
KW technetium-99m; radiolabelled; Gp IIb/IIIa receptor ligand.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "(S-benzoyl-2-mercaptoacetyl)-Gly"
XX
PN WO9323085-A.
XX
PD 25-NOV-1993.
XX
PF 21-MAY-1993; 93WO-US04794.
XX
PR 21-MAY-1992; 92US-0886752.
XX
PA (DIAT-) DIATECH INC.
XX
PI Dean RT, Lister-James J;
XX
DR WPI; 1993-386229/48.
XX
PT Reagent for scintigraphic imaging of thrombi with 99m technetium
PT - comprises synthetic peptide which binds to thrombus, covalently
PT coupled to metal binding gp.; rapidly cleared from blood and
PT tissue
XX
PS Claim 41; Page 46; 61pp; English.
XX
CC The invention relates to reagents for scintigraphic imaging of a
CC thrombus in-vivo, comprising (A) a specific binding compound capable of
CC binding to at least one component of a thrombus, covaleptly linked
CC to (B) a technetium-99m-binding moiety. Specific peptides
CC constituting the reagents are claimed as new. The present peptide is
CC one such peptide.
XX
SQ Sequence 6 AA;

Query Match 87.9%; Score 29; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRGDF 5
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Db 2 grgdf 6

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GenCore version 4.5

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Title: US-09-081-522-4
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Searched: 174772 seqs, 17957048 residues

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Maximum DB seq length: 6

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	33	100.0	6	1	US-08-210-715-2	Sequence 2, Appli
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4	33	100.0	6	1	US-08-210-715-4	Sequence 4, Appli
5	33	100.0	6	1	US-08-366-665-1	Sequence 1, Appli
6	33	100.0	6	1	US-08-366-665-2	Sequence 2, Appli
7	33	100.0	6	1	US-08-366-665-3	Sequence 3, Appli
8	33	100.0	6	1	US-08-366-665-4	Sequence 4, Appli
9	30	90.9	6	1	US-08-210-715-11	Sequence 11, Appl
10	30	90.9	6	1	US-08-366-665-11	Sequence 11, Appl
11	29	87.9	5	5	5330911-13	Patent No. 5330911
12	29	87.9	6	1	US-08-482-880-21	Sequence 21, Appl
13	29	87.9	6	1	US-08-482-880-25	Sequence 25, Appl
14	29	87.9	6	2	US-08-273-274-21	Sequence 21, Appl
15	29	87.9	6	2	US-08-273-274-25	Sequence 25, Appl
16	29	87.9	6	2	US-08-475-041-21	Sequence 21, Appl
17	29	87.9	6	2	US-08-475-041-25	Sequence 25, Appl
18	29	87.9	6	2	US-08-335-832-21	Sequence 21, Appl
19	29	87.9	6	2	US-08-335-832-22	Sequence 22, Appl
20	29	87.9	6	2	US-08-753-781-16	Sequence 16, Appl
21	29	87.9	6	2	US-08-484-773-21	Sequence 21, Appl
22	29	87.9	6	2	US-08-484-773-25	Sequence 25, Appl
23	29	87.9	6	2	US-08-361-864-25	Sequence 25, Appl
24	27	81.8	5	1	US-08-210-715-5	Sequence 5, Appli
25	27	81.8	5	1	US-08-210-715-7	Sequence 7, Appli
26	27	81.8	5	1	US-08-366-665-5	Sequence 5, Appli
27	27	81.8	5	1	US-08-366-665-7	Sequence 7, Appli
28	27	81.8	5	2	US-08-616-770-2	Sequence 2, Appli
29	26	78.8	5	1	US-08-234-034-1	Sequence 1, Appli
30	26	78.8	5	5	5330911-3	Patent No. 5330911
31	26	78.8	5	5	5330911-6	Patent No. 5330911
32	24	72.7	6	1	US-08-210-715-10	Sequence 10, Appl
33	24	72.7	6	1	US-08-366-665-10	Sequence 10, Appl
34	23	69.7	4	1	US-07-932-200-10	Sequence 10, Appl
35	23	69.7	4	1	US-08-109-106-6	Sequence 6, Appli
36	23	69.7	4	1	US-08-461-611-36	Sequence 36, Appl
37	23	69.7	4	1	US-08-596-116A-68	Sequence 68, Appl
38	23	69.7	4	2	US-08-668-871-12	Sequence 12, Appl
39	23	69.7	4	2	US-08-669-683-12	Sequence 12, Appl
40	23	69.7	4	2	US-08-387-749-10	Sequence 10, Appl
41	23	69.7	4	2	US-08-623-833B-5	Sequence 5, Appli
42	23	69.7	4	2	US-08-335-832-25	Sequence 25, Appl
43	23	69.7	4	2	US-08-747-137-69	Sequence 69, Appl
44	23	69.7	4	2	US-08-753-781-20	Sequence 20, Appl
45	23	69.7	4	2	US-08-361-864-28	Sequence 28, Appl

ALIGNMENTS

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RESULT 1
US-08-210-715-1
; Sequence 1, Application US/08210715
; Patent No. 5753230
; GENERAL INFORMATION:
;   APPLICANT: Brooks, Peter
;   APPLICANT: Cheresh, David A
;   TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR
;   TITLE OF INVENTION: INHIBITION OF ANGIOGENESIS
;   NUMBER OF SEQUENCES: 14
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Office of Patent Counsel, The Scripps
;     ADDRESSEE: Research Institute
;     STREET: 10666 No. 5753230th Torrey Pines Road, TPC-8
;     CITY: La Jolla
;     STATE: CA
;     COUNTRY: USA
;     ZIP: 92037
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/210,715
;     FILING DATE: 18-MAR-1994
;     CLASSIFICATION: 514
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Fitting, Thomas
;     REGISTRATION NUMBER: 34,163
;     REFERENCE/DOCKET NUMBER: TSRI 419.0
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (619) 554-2937
;     TELEFAX: (619) 554-6312
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 6 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   FRAGMENT TYPE: internal
;   FEATURE:
;     NAME/KEY: Peptide
;     LOCATION: 1..6
;     OTHER INFORMATION: /label= BOC-GRGDFV-OMe
;     OTHER INFORMATION: /note= "BOC signifies the N-terminal protecting
;     OTHER INFORMATION: group butyloxycarbonyl; OMe signifies a C-terminal
;     OTHER INFORMATION: methyl ester; arginine in the second position
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;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  1..6
;      OTHER INFORMATION:  /label= OMe
;      OTHER INFORMATION:  /note= "OMe signifies the C-terminal protecting
;      OTHER INFORMATION:  group methyl ester."
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;      OTHER INFORMATION:  /note= "A prefix "D" in D-Arg signifies that the
;      OTHER INFORMATION:  arginine in position 2 is a D-amino acid."
US-08-210-715-1


  Query Match             100.0%;  Score 33;  DB 1;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GRGDFV 6
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Db      1 GRGDFV 6


RESULT   2
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; Sequence 2, Application US/08210715
; Patent No. 5753230
;  GENERAL INFORMATION:
;    APPLICANT:  Brooks, Peter
;    APPLICANT:  Cheresh, David A
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS USEFUL FOR
;    TITLE OF INVENTION:  INHIBITION OF ANGIOGENESIS
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Office of Patent Counsel, The Scripps
;      ADDRESSEE:  Research Institute
;      STREET:  10666 No. 5753230th Torrey Pines Road, TPC-8
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/210,715
;      FILING DATE:  18-MAR-1994
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fitting, Thomas
;      REGISTRATION NUMBER:  34,163
;      REFERENCE/DOCKET NUMBER:  TSRI 419.0
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 554-2937
;      TELEFAX:  (619) 554-6312
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
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;    FEATURE:
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;      OTHER INFORMATION:  /label= BOC
;      OTHER INFORMATION:  /note= "BOC signifies the N-terminal blocking
;      OTHER INFORMATION:  group tertbutyloxycarbonyl."
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;      NAME/KEY:  Peptide
;      LOCATION:  1..6
;      OTHER INFORMATION:  /label= OH
;      OTHER INFORMATION:  /note= "OH signifies a free C-terminal carboxylic
;      OTHER INFORMATION:  acid."
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  1..6
;      OTHER INFORMATION:  /label= D-Arg
;      OTHER INFORMATION:  /note= "A prefix "D" in D-Arg signifies that the
;      OTHER INFORMATION:  arginine in position 2 is a D-amino acid."
US-08-210-715-2


  Query Match             100.0%;  Score 33;  DB 1;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GRGDFV 6
          ||||||
Db      1 GRGDFV 6


RESULT   3
US-08-210-715-3
; Sequence 3, Application US/08210715
; Patent No. 5753230
;  GENERAL INFORMATION:
;    APPLICANT:  Brooks, Peter
;    APPLICANT:  Cheresh, David A
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS USEFUL FOR
;    TITLE OF INVENTION:  INHIBITION OF ANGIOGENESIS
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Office of Patent Counsel, The Scripps
;      ADDRESSEE:  Research Institute
;      STREET:  10666 No. 5753230th Torrey Pines Road, TPC-8
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/210,715
;      FILING DATE:  18-MAR-1994
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fitting, Thomas
;      REGISTRATION NUMBER:  34,163
;      REFERENCE/DOCKET NUMBER:  TSRI 419.0
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 554-2937
;      TELEFAX:  (619) 554-6312
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  internal
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  1..6
;      OTHER INFORMATION:  /label= H
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;      OTHER INFORMATION:  /note= "H signifies a free N-terminal amine."
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  1..6
;      OTHER INFORMATION:  /label= OH
;      OTHER INFORMATION:  /note= "OH signifies a free C-terminal carboxylic
;      OTHER INFORMATION:  acid."
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  1..6
;      OTHER INFORMATION:  /label= D-Arg
;      OTHER INFORMATION:  /note= "A prefix "D" in D-Arg at position 2,
;      OTHER INFORMATION:  signifies that the arginine is a D-amino acid."
US-08-210-715-3


  Query Match             100.0%;  Score 33;  DB 1;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GRGDFV 6
          ||||||
Db      1 GRGDFV 6


RESULT   4
US-08-210-715-4
; Sequence 4, Application US/08210715
; Patent No. 5753230
;  GENERAL INFORMATION:
;    APPLICANT:  Brooks, Peter
;    APPLICANT:  Cheresh, David A
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS USEFUL FOR
;    TITLE OF INVENTION:  INHIBITION OF ANGIOGENESIS
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Office of Patent Counsel, The Scripps
;      ADDRESSEE:  Research Institute
;      STREET:  10666 No. 5753230th Torrey Pines Road, TPC-8
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/210,715
;      FILING DATE:  18-MAR-1994
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fitting, Thomas
;      REGISTRATION NUMBER:  34,163
;      REFERENCE/DOCKET NUMBER:  TSRI 419.0
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 554-2937
;      TELEFAX:  (619) 554-6312
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  internal
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  1..6
;      OTHER INFORMATION:  /label= cyclo
;      OTHER INFORMATION:  /note= "Cyclo signifies a cyclic peptide; lower
;      OTHER INFORMATION:  case letters indicate a D-amino acid; capital
;      OTHER INFORMATION:  letters indicate a L-amino acid."
US-08-210-715-4


  Query Match             100.0%;  Score 33;  DB 1;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GRGDFV 6
          ||||||
Db      1 GRGDFV 6


RESULT   5
US-08-366-665-1
; Sequence 1, Application US/08366665
; Patent No. 5766591
;  GENERAL INFORMATION:
;    APPLICANT:  Brooks, Peter
;    APPLICANT:  Cheresh, David A
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS USEFUL FOR
;    TITLE OF INVENTION:  INHIBITION OF ANGIOGENESIS
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Office of Patent Counsel, The Scripps
;      ADDRESSEE:  Research Institute
;      STREET:  10666 No. 5766591th Torrey Pines Road, TPC-8
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/366,665
;      FILING DATE:  30-DEC-1994
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/210,715
;      FILING DATE:  18-MAR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fitting, Thomas
;      REGISTRATION NUMBER:  34,163
;      REFERENCE/DOCKET NUMBER:  TSRI 419.1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 554-2937
;      TELEFAX:  (619) 554-6312
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  internal
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  1..6
;      OTHER INFORMATION:  /label= BOC-GRGDFV-OMe
;      OTHER INFORMATION:  /note= "BOC signifies the N-terminal protecting
;      OTHER INFORMATION:  group butyloxycarbonyl; OMe signifies a C-terminal
;      OTHER INFORMATION:  methyl ester;  arginine in the second position
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  1..6
;      OTHER INFORMATION:  /label= OMe
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;      OTHER INFORMATION:  /note= "OMe signifies the C-terminal protecting
;      OTHER INFORMATION:  group methyl ester."
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  1..6
;      OTHER INFORMATION:  /label= D-Arg
;      OTHER INFORMATION:  /note= "A prefix "D" in D-Arg signifies that the
;      OTHER INFORMATION:  arginine in position 2 is a D-amino acid."
US-08-366-665-1


  Query Match           100.0%;  Score 33;  DB 1;  Length 6;
  Best Local Similarity  100.0%;  Pred. No. 1.3e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GRGDFV 6
          ||||||
Db      1 GRGDFV 6


RESULT   6
US-08-366-665-2
; Sequence 2, Application US/08366665
; Patent No. 5766591
;  GENERAL INFORMATION:
;    APPLICANT:  Brooks, Peter
;    APPLICANT:  Cheresh, David A
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS USEFUL FOR
;    TITLE OF INVENTION:  INHIBITION OF ANGIOGENESIS
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Office of Patent Counsel, The Scripps
;      ADDRESSEE:  Research Institute
;      STREET:  10666 No. 5766591th Torrey Pines Road, TPC-8
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/366,665
;      FILING DATE:  30-DEC-1994
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/210,715
;      FILING DATE:  18-MAR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fitting, Thomas
;      REGISTRATION NUMBER:  34,163
;      REFERENCE/DOCKET NUMBER:  TSRI 419.1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 554-2937
;      TELEFAX:  (619) 554-6312
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  internal
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  1..6
;      OTHER INFORMATION:  /label= BOC
;      OTHER INFORMATION:  /note= "BOC signifies the N-terminal blocking
;      OTHER INFORMATION:  group tertbutyloxycarbonyl."
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  1..6
;      OTHER INFORMATION:  /label= OH
;      OTHER INFORMATION:  /note= "OH signifies a free C-terminal carboxylic
;      OTHER INFORMATION:  acid."
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  1..6
;      OTHER INFORMATION:  /label= D-Arg
;      OTHER INFORMATION:  /note= "A prefix "D" in D-Arg signifies that the
;      OTHER INFORMATION:  arginine in position 2 is a D-amino acid."
US-08-366-665-2


  Query Match           100.0%;  Score 33;  DB 1;  Length 6;
  Best Local Similarity  100.0%;  Pred. No. 1.3e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GRGDFV 6
          ||||||
Db      1 GRGDFV 6


RESULT   7
US-08-366-665-3
; Sequence 3, Application US/08366665
; Patent No. 5766591
;  GENERAL INFORMATION:
;    APPLICANT:  Brooks, Peter
;    APPLICANT:  Cheresh, David A
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS USEFUL FOR
;    TITLE OF INVENTION:  INHIBITION OF ANGIOGENESIS
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Office of Patent Counsel, The Scripps
;      ADDRESSEE:  Research Institute
;      STREET:  10666 No. 5766591th Torrey Pines Road, TPC-8
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/366,665
;      FILING DATE:  30-DEC-1994
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/210,715
;      FILING DATE:  18-MAR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fitting, Thomas
;      REGISTRATION NUMBER:  34,163
;      REFERENCE/DOCKET NUMBER:  TSRI 419.1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 554-2937
;      TELEFAX:  (619) 554-6312
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  internal
;    FEATURE:
;      NAME/KEY:  Peptide
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;     LOCATION:  1..6
;     OTHER INFORMATION:  /label= H
;     OTHER INFORMATION:  /note= "H signifies a free N-terminal amine."
;   FEATURE:
;     NAME/KEY:  Peptide
;     LOCATION:  1..6
;     OTHER INFORMATION:  /label= OH
;     OTHER INFORMATION:  /note= "OH signifies a free C-terminal carboxylic
;     OTHER INFORMATION:  acid."
;   FEATURE:
;     NAME/KEY:  Peptide
;     LOCATION:  1..6
;     OTHER INFORMATION:  /label= D-Arg
;     OTHER INFORMATION:  /note= "A prefix "D" in D-Arg at position 2,
;     OTHER INFORMATION:  signifies that the arginine is a D-amino acid."
US-08-366-665-3


  Query Match             100.0%;  Score 33;  DB 1;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GRGDFV 6
          ||||||
Db      1 GRGDFV 6


RESULT   8
US-08-366-665-4
; Sequence 4, Application US/08366665
; Patent No. 5766591
;  GENERAL INFORMATION:
;    APPLICANT:  Brooks, Peter
;    APPLICANT:  Cheresh, David A
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS USEFUL FOR
;    TITLE OF INVENTION:  INHIBITION OF ANGIOGENESIS
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Office of Patent Counsel, The Scripps
;      ADDRESSEE:  Research Institute
;      STREET:  10666 No. 5766591th Torrey Pines Road, TPC-8
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/366,665
;      FILING DATE:  30-DEC-1994
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/210,715
;      FILING DATE:  18-MAR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fitting, Thomas
;      REGISTRATION NUMBER:  34,163
;      REFERENCE/DOCKET NUMBER:  TSRI 419.1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 554-2937
;      TELEFAX:  (619) 554-6312
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  internal
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  1..6
;      OTHER INFORMATION:  /label= cyclo
;      OTHER INFORMATION:  /note= "Cyclo signifies a cyclic peptide; lower
;      OTHER INFORMATION:  case letters inidcate a D-amino acid; capital
;      OTHER INFORMATION:  letters indicate a L-amino acid."
US-08-366-665-4


  Query Match             100.0%;  Score 33;  DB 1;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GRGDFV 6
          ||||||
Db      1 GRGDFV 6


RESULT   9
US-08-210-715-11
; Sequence 11, Application US/08210715
; Patent No. 5753230
;  GENERAL INFORMATION:
;    APPLICANT:  Brooks, Peter
;    APPLICANT:  Cheresh, David A
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS USEFUL FOR
;    TITLE OF INVENTION:  INHIBITION OF ANGIOGENESIS
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Office of Patent Counsel, The Scripps
;      ADDRESSEE:  Research Institute
;      STREET:  10665 No. 5753230th Torrey Pines Road, TPC-8
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/210,715
;      FILING DATE:  18-MAR-1994
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fitting, Thomas
;      REGISTRATION NUMBER:  34,163
;      REFERENCE/DOCKET NUMBER:  TSRI 419.0
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 554-2937
;      TELEFAX:  (619) 554-6312
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  internal
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  1..6
;      OTHER INFORMATION:  /label= cyclo
;      OTHER INFORMATION:  /note= "Cyclo signifies a cyclic peptide; lower
;      OTHER INFORMATION:  case letters indicate a D-amino acid; capital
;      OTHER INFORMATION:  letters indicate a L-amino acid."
US-08-210-715-11
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  Query Match             90.9%;  Score 30;  DB 1;  Length 6;
  Best Local Similarity   83.3%;  Pred. No. 1.3e+05;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GRGDFV 6
          |||||:
Db      1 GRGDFL 6


RESULT  10
US-08-366-665-11
; Sequence 11, Application US/08366665
; Patent No. 5766591
;  GENERAL INFORMATION:
;    APPLICANT:  Brooks, Peter
;    APPLICANT:  Cheresh, David A
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS USEFUL FOR
;    TITLE OF INVENTION:  INHIBITION OF ANGIOGENESIS
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Office of Patent Counsel, The Scripps
;      ADDRESSEE:  Research Institute
;      STREET:  10666 No. 5766591th Torrey Pines Road, TPC-8
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/366,665
;      FILING DATE:  30-DEC-1994
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/210,715
;      FILING DATE:  18-MAR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fitting, Thomas
;      REGISTRATION NUMBER:  34,163
;      REFERENCE/DOCKET NUMBER:  TSRI 419.1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 554-2937
;      TELEFAX:  (619) 554-6312
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  internal
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  1..6
;      OTHER INFORMATION:  /label= cyclo
;      OTHER INFORMATION:  /note= "Cyclo signifies a cyclic peptide; lower
;      OTHER INFORMATION:  case letters indicate a D-amino acid; capital
;      OTHER INFORMATION:  letters indicate a L-amino acid."
US-08-366-665-11


  Query Match             90.9%;  Score 30;  DB 1;  Length 6;
  Best Local Similarity   83.3%;  Pred. No. 1.3e+05;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GRGDFV 6
          |||||:
Db      1 GRGDFL 6


RESULT  11
5330911-13
;Patent No. 5330911
;    APPLICANT: HUBBELL, JEFFREY A.;MASSIA, STEPHEN P.;DESAI,
;NEIL P.
;    TITLE OF INVENTION: SURFACES HAVING DESIRABLE CELL
;ADHESIVE EFFECTS
;    NUMBER OF SEQUENCES: 27
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/527,198
;      FILING DATE: 21-MAY-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 414,144
;      FILING DATE: 28-SEP-1989
;SEQ ID NO:13:
;      LENGTH: 5
5330911-13


  Query Match             87.9%;  Score 29;  DB 5;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GRGDF 5
          |||||
Db      1 GRGDF 5


RESULT  12
US-08-482-880-21
; Sequence 21, Application US/08482880
; Patent No. 5736122
;  GENERAL INFORMATION:
;    APPLICANT:  Dean, Richard T
;    APPLICANT:  Lister-James, John
;    TITLE OF INVENTION:  Technetium-99m Labeled Peptides for
;    TITLE OF INVENTION:  Thrombus Imaging
;    NUMBER OF SEQUENCES:  33
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Banner & Allegretti, Ltd.
;      STREET:  10 South Wacker Drive Suite 3000
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,880
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5736122nan, Kevin E
;      REGISTRATION NUMBER:  35,303
;      REFERENCE/DOCKET NUMBER:  92,216-L
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-715-1000
;      TELEFAX:  312-715-1234
;      TELEX:  910-221-5317
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-482-880-21
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  Query Match             87.9%;  Score 29;  DB 1;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GRGDF 5
          |||||
Db      2 GRGDF 6


RESULT 13
US-08-482-880-25
; Sequence 25, Application US/08482880
; Patent No. 5736122
;  GENERAL INFORMATION:
;    APPLICANT:  Dean, Richard T
;    APPLICANT:  Lister-James, John
;    TITLE OF INVENTION:  Technetium-99m Labeled Peptides for
;    TITLE OF INVENTION:  Thrombus Imaging
;    NUMBER OF SEQUENCES:  33
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Banner & Allegretti, Ltd.
;      STREET:  10 South Wacker Drive Suite 3000
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,880
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5736122nan, Kevin E
;      REGISTRATION NUMBER:  35,303
;      REFERENCE/DOCKET NUMBER:  92,216-L
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-715-1000
;      TELEFAX:  312-715-1234
;      TELEX:  910-221-5317
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-482-880-25


  Query Match             87.9%;  Score 29;  DB 1;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GRGDF 5
          |||||
Db      2 GRGDF 6


RESULT 14
US-08-273-274-21
; Sequence 21, Application US/08273274
; Patent No. 5849260
;  GENERAL INFORMATION:
;    APPLICANT:  Dean, Richard T
;    APPLICANT:  Lister-James, John
;    TITLE OF INVENTION:  Technetium-99m Labeled Peptides for
;    TITLE OF INVENTION:  Thrombus Imaging
;    NUMBER OF SEQUENCES:  33
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Allegretti & Witcoff, Ltd.
;      STREET:  10 South Wacker Drive Suite 3000
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/273,274
;      FILING DATE:
;      CLASSIFICATION:  436
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/886,752
;      FILING DATE:  21-MAY-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5849260nan, Kevin E
;      REGISTRATION NUMBER:  35,303
;      REFERENCE/DOCKET NUMBER:  92,216
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-715-1000
;      TELEFAX:  312-715-1234
;      TELEX:  910-221-5317
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-273-274-21


  Query Match             87.9%;  Score 29;  DB 2;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GRGDF 5
          |||||
Db      2 GRGDF 6


RESULT 15
US-08-273-274-25
; Sequence 25, Application US/08273274
; Patent No. 5849260
;  GENERAL INFORMATION:
;    APPLICANT:  Dean, Richard T
;    APPLICANT:  Lister-James, John
;    TITLE OF INVENTION:  Technetium-99m Labeled Peptides for
;    TITLE OF INVENTION:  Thrombus Imaging
;    NUMBER OF SEQUENCES:  33
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Allegretti & Witcoff, Ltd.
;      STREET:  10 South Wacker Drive Suite 3000
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/273,274
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/886,752
;      FILING DATE:  21-MAY-1992
```

; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5849260nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,216
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-273-274-25

Query Match 87.9%; Score 29; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 GRGDF 5
          |||||
Db      2 GRGDF 6
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Search completed: March 6, 2001, 09:42:36
Job time: 18 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: March 6, 2001, 09:42:22 ; Search time 13.62 Seconds
(without alignments)
29.912 Million cell updates/sec

Title: US-09-081-522-4
Perfect score: 33
Sequence: 1 GRGDFV 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 315

Minimum DB seq length: 0
Maximum DB seq length: 6

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_66:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	17	51.5	5	2	PT0608	T-cell receptor be
2	17	51.5	6	2	I51434	H4 histone - Afric
3	13	39.4	6	2	PT0629	T-cell receptor be
4	13	39.4	6	2	PT0514	T-cell receptor be
5	13	39.4	6	2	A43129	neuropeptide GNFFR
6	12	36.4	4	2	PT0711	T-cell receptor be
7	12	36.4	5	2	A32516	cholecystokinin-5
8	12	36.4	5	2	PQ0689	photosystem I 10.4
9	12	36.4	5	2	A44692	fulicin - giant Af
10	12	36.4	5	2	B61445	Leu-enkephalin - b
11	12	36.4	5	2	A61445	Met-enkephalin - b
12	12	36.4	5	2	PT0513	T-cell receptor be
13	12	36.4	5	2	PT0538	T-cell receptor be
14	12	36.4	5	2	PT0703	T-cell receptor be
15	12	36.4	5	2	PT0690	T-cell receptor be
16	12	36.4	5	2	PT0573	T-cell receptor be
17	12	36.4	5	2	PT0679	T-cell receptor be
18	12	36.4	6	2	PT0511	T-cell receptor be
19	12	36.4	6	2	PT0604	T-cell receptor be
20	12	36.4	6	2	PT0630	T-cell receptor be
21	12	36.4	6	2	PT0687	T-cell receptor be
22	12	36.4	6	2	PT0652	T-cell receptor be
23	12	36.4	6	2	PT0587	T-cell receptor be
24	12	36.4	6	2	PT0558	T-cell receptor be
25	12	36.4	6	2	PT0709	T-cell receptor be
26	12	36.4	6	2	PD0028	pev-kinin 2 - pena
27	11	33.3	4	1	ECXAA	antho-RFamide neur
28	11	33.3	4	2	A25844	autho-RF amide neu
29	11	33.3	4	2	S39390	myosin-light-chain
30	11	33.3	4	2	S47552	ubiquitin - rat
31	11	33.3	5	2	C23751	spinal cord peptid
32	11	33.3	5	2	I40702	primase - Citrobac
33	11	33.3	5	2	B61168	cocoonase (EC 3.4.
34	11	33.3	5	2	S53595	hypothetical prote
35	11	33.3	5	2	D44823	synaptosomal-assoc
36	11	33.3	5	2	C53284	T-cell receptor be
37	11	33.3	5	2	PT0525	T-cell receptor be
38	11	33.3	5	2	PT0553	T-cell receptor be
39	11	33.3	5	2	PT0695	T-cell receptor be
40	11	33.3	5	2	PT0700	T-cell receptor be
41	11	33.3	6	2	A60494	antineoplastic gly
42	11	33.3	6	2	PT0280	Ig heavy chain CRD
43	11	33.3	6	2	PT0605	T-cell receptor be
44	11	33.3	6	2	PT0641	T-cell receptor be
45	11	33.3	6	2	PT0668	T-cell receptor be

ALIGNMENTS

RESULT 1
PT0608
T-cell receptor beta chain V-D-J region (120-2CF) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0608
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A;Reference number: PT0509; MUID:91277601
A;Accession: PT0608
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <FEE>
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 51.5%; Score 17; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 GRG 3
          |||
Db      3 GRG 5
```

RESULT 2
I51434
H4 histone - African clawed frog (fragment)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: I51434
R;Woodland, H.R.; Warmington, J.R.; Ballantine, J.E.M.; Turner, P.C.
Nucleic Acids Res. 12, 4939-4958, 1984
A;Title: Are there major developmentally regulated H4 gene classes in Xenopus?.
A;Reference number: I51391; MUID:84247348
A;Accession: I51434
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-6 <WOO>
A;Cross-references: GB:K02304; NID:g214227; PIDN:AAA49738.1; PID:g555517

Query Match 51.5%; Score 17; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 GRG 3
          |||
Db      3 GRG 5
```

```
RESULT   3
PT0629
T-cell receptor beta chain V-D-J region (100-2AH) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0629; PT0528
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601
A;Accession: PT0629
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-6 <FEE>
A;Experimental source: newborn thymus, strain BALB/c, clone 100-2AH
A;Accession: PT0528
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-6 <FE2>
A;Experimental source: adult thymus, strain BALB/c, clone 100-4AB
C;Keywords: T-cell receptor

  Query Match             39.4%;  Score 13;  DB 2;  Length 6;
  Best Local Similarity   66.7%;  Pred. No. 2e+05;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 GDF 5
           ||:
Db       3 GDW 5

RESULT   4
PT0514
T-cell receptor beta chain V-D-J region (100-4AC) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0514
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601
A;Accession: PT0514
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-6 <FEE>
A;Experimental source: adult thymus, strain BALB/c
C;Keywords: T-cell receptor

  Query Match             39.4%;  Score 13;  DB 2;  Length 6;
  Best Local Similarity   66.7%;  Pred. No. 2e+05;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GRG 3
           |:|
Db       4 GQG 6

RESULT   5
A43129
neuropeptide GNFFRFamide - tapeworm (Moniezia expansa)
C;Species: Moniezia expansa
C;Date: 10-Nov-1997 #sequence_revision 14-Nov-1997 #text_change 14-Nov-1997
C;Accession: A43129
R;Maule, A.; Shaw, C.; Halton, D.; Thim, L.
Biochem. Biophys. Res. Commun. 193, 1054-1060, 1993
A;Title: GNFFRFamide: A novel FMRFamide-immunoreactive peptide isolated from the sheep t
A;Reference number: A43129; MUID:93312289
A;Accession: A43129
A;Molecule type: protein
A;Residues: 1-6 <MAU>
C;Keywords: amidated carboxyl end; neuropeptide
F;6/Modified site: amidated carboxyl end (Phe) #status predicted

  Query Match             39.4%;  Score 13;  DB 2;  Length 6;
  Best Local Similarity   66.7%;  Pred. No. 2e+05;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 GDF 5
           |:|
Db       1 GNF 3

RESULT   6
PT0711
T-cell receptor beta chain V-D-J region (120-2J) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0607; PT0674; PT0678; PT0570; PT0711; PT0710
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A;Reference number: PT0509; MUID:91277601
A;Accession: PT0607
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-4 <FE1>
A;Experimental source: newborn thymus, strain BALB/c, 120-2J
A;Accession: PT0674
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-4 <FE2>
A;Experimental source: day 18 fetal thymus, strain BALB/c, 140-1G
A;Accession: PT0678
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-4 <FE3>
A;Experimental source: day 18 fetal thymus, strain BALB/c, 154-1L
A;Accession: PT0570
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-4 <FE4>
A;Experimental source: day 19 fetal thymus, strain BALB/c, 141-1I
A;Accession: PT0711
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-4 <FE5>
A;Experimental source: newborn thymus, strain BALB/c (clones 161-2AE and 161-2AF)
C;Keywords: T-cell receptor

  Query Match             36.4%;  Score 12;  DB 2;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 2e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 GD 4
           ||
Db       3 GD 4

RESULT   7
A32516
cholecystokinin-5 - dog
N;Alternate names: CCK-5
C;Species: Canis lupus familiaris (dog)
C;Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 18-Aug-2000
C;Accession: A32516
R;Shively, J.; Reeve Jr., J.R.; Eysselein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, J
Am. J. Physiol. 252, G272-G275, 1987
A;Title: CCK-5: sequence analysis of a small cholecystokinin from canine brain and in
A;Reference number: A32516; MUID:87153871
A;Accession: A32516
A;Molecule type: protein
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A;Residues: 1-5 <SHI>
C;Comment: This peptide corresponds to the five carboxyl-terminal residues of cholecysto
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; neuropeptide
F;5/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 36.4%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DF 5
||
Db 4 DF 5

RESULT 8
PQ0689
photosystem I 10.4K H1 chain - common tobacco (fragment)
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 17-Mar-1999
C;Accession: PQ0689
R;Obokata, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugiura, M.
Plant Physiol. 102, 1259-1267, 1993
A;Title: Molecular heterogeneity of photosystem I. psaD, psaE, psaF, psaH and psaL are a
A;Reference number: PQ0667; MUID:94105345
A;Accession: PQ0689
A;Molecule type: protein
A;Residues: 1-5 <OBO>
C;Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match 36.4%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GD 4
||
Db 3 GD 4

RESULT 9
A44692
fulicin - giant African snail
C;Species: Achatina fulica (giant African snail)
C;Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 11-Jul-1997
C;Accession: A44692
R;Ohta, N.; Kubota, I.; Takao, T.; Shimonishi, Y.; Yasuda-Kamatani, Y.; Minakata, H.; Nc
Biochem. Biophys. Res. Commun. 178, 486-493, 1991
A;Title: Fulicin, a novel neuropeptide containing a D-amino acid residue isolated from t
A;Reference number: A44692; MUID:91315471
A;Accession: A44692
A;Molecule type: protein
A;Residues: 1-5 <OHT>
C;Keywords: amidated carboxyl end; D-amino acid; neuropeptide
F;2/Modified site: D-asparagine (Asn) #status experimental
F;5/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 36.4%; Score 12; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DFV 6
:||
Db 3 EFV 5

RESULT 10
B61445
Leu-enkephalin - blue mussel
C;Species: Mytilus edulis (blue mussel)
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 21-Jan-2000
C;Accession: B61445
R;Leung, M.K.; Stefano, G.B.
Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984
A;Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edul
A;Reference number: A61445; MUID:84144823
A;Accession: B61445
A;Molecule type: protein
A;Residues: 1-5 <LEU>
A;Experimental source: pedal ganglia
C;Keywords: neuropeptide; opioid peptide

Query Match 36.4%; Score 12; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GDFV 6
| |:
Db 2 GGFL 5

RESULT 11
A61445
Met-enkephalin - blue mussel
C;Species: Mytilus edulis (blue mussel)
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 21-Jan-2000
C;Accession: A61445
R;Leung, M.K.; Stefano, G.B.
Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984
A;Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edul
A;Reference number: A61445; MUID:84144823
A;Accession: A61445
A;Molecule type: protein
A;Residues: 1-5 <LEU>
A;Experimental source: pedal ganglia
C;Keywords: neuropeptide; opioid peptide

Query Match 36.4%; Score 12; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GDFV 6
| |:
Db 2 GGFM 5

RESULT 12
PT0513
T-cell receptor beta chain V-D-J region (100-4AL) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0513; PT0606
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A;Reference number: PT0509; MUID:91277601
A;Accession: PT0513
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <FEE>
A;Experimental source: adult thymus, strain BALB/c, clone 100-4AL
A;Accession: PT0606
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <FE2>
A;Experimental source: newborn thymus, strain BALB/c, clone 120-1S
C;Keywords: T-cell receptor

Query Match 36.4%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      3 GD 4
          ||
Db      3 GD 4


RESULT  13
PT0538
T-cell receptor beta chain V-D-J region (126-1F) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0538; PT0539; PT0603
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601
A;Accession: PT0538
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <FEE>
A;Experimental source: day 18 fetal thymus, strain BALB/c, clone 126-1F
A;Accession: PT0539
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <FE3>
A;Experimental source: day 18 fetal thymus, strain BALB/c, clone 126-1H
A;Accession: PT0603
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <FE2>
A;Experimental source: newborn thymus, strain BALB/c, clone 100-2AC
C;Keywords: T-cell receptor


  Query Match             36.4%;  Score 12;  DB 2;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 2e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 GD 4
          ||
Db      3 GD 4


RESULT  14
PT0703
T-cell receptor beta chain V-D-J region (135-1F) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0703
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601
A;Accession: PT0703
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-5 <FEE>
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor


  Query Match             36.4%;  Score 12;  DB 2;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 2e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 GD 4
          ||
Db      3 GD 4


RESULT  15
PT0690
T-cell receptor beta chain V-D-J region (140-1BD) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0690
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A;Reference number: PT0509; MUID:91277601
A;Accession: PT0690
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-5 <FEE>
A;Experimental source: day 18 fetal thymus, strain BALB/c
C;Keywords: T-cell receptor


  Query Match             36.4%;  Score 12;  DB 2;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 2e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 GD 4
          ||
Db      3 GD 4


Search completed: March  6, 2001, 09:43:11
Job time: 49 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: March 6, 2001, 09:42:41 ; Search time 8.47 Seconds
(without alignments)
22.877 Million cell updates/sec

Title: US-09-081-522-4
Perfect score: 33
Sequence: 1 GRGDFV 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 38

Minimum DB seq length: 0
Maximum DB seq length: 6

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	13	39.4	6	1	FARP_MONEX	P41966 moniezia ex
2	12	36.4	5	1	UXA4_CHLTR	P38005 chlamydia t
3	11	33.3	5	1	UF01_MOUSE	P38639 mus musculu
4	10	30.3	5	1	TPIS_CANFA	P54714 canis famil
5	10	30.3	6	1	CIP1_MYTED	P13736 mytilus edu
6	10	30.3	6	1	CIP2_MYTED	P13737 mytilus edu
7	9	27.3	4	1	ACH1_ACHFU	P35904 achatina fu
8	9	27.3	5	1	PAP2_PARMA	P81864 pardachirus
9	8	24.2	5	1	TRM3_ECOLI	P13973 escherichia
10	7	21.2	4	1	FLRF_HIRME	P42561 hirudo medi
11	7	21.2	4	1	FMRF_MACNI	P01162 macrocallis
12	6	18.2	3	1	GRWM_HUMAN	P01157 homo sapien
13	6	18.2	3	1	LUXE_VIBFI	P24272 vibrio fisc
14	6	18.2	4	1	DCML_PSECH	P19916 pseudomonas
15	6	18.2	4	1	EOSI_HUMAN	P02731 homo sapien
16	6	18.2	4	1	FAR3_HIRME	P42562 hirudo medi
17	6	18.2	4	1	FAR4_HIRME	P42563 hirudo medi
18	6	18.2	5	1	AL14_CARMA	P81817 carcinus ma
19	6	18.2	5	1	BIOA_CITFR	P13071 citrobacter
20	6	18.2	5	1	BIOA_SALTY	P12677 salmonella
21	6	18.2	5	1	FARP_ARTTR	P41853 artioposthi
22	6	18.2	5	1	SUGA_ACHDO	P19991 acheta dome
23	6	18.2	5	1	UC22_MAIZE	P80628 zea mays (m
24	6	18.2	6	1	LOK1_LOCMI	P41491 locusta mig
25	6	18.2	6	1	TRPI_PSEPU	P36414 pseudomonas
26	5	15.2	4	1	TUFT_HUMAN	P01858 homo sapien
27	5	15.2	5	1	BIOB_SALTY	P12678 salmonella
28	5	15.2	5	1	PRCT_PERAM	P01373 periplaneta
29	5	15.2	6	1	ACPH_RABIT	P25154 oryctolagus
30	4	12.1	4	1	RM01_YEAST	P36515 saccharomyc
31	3	9.1	6	1	OVM_LEPDE	P42985 leptinotars
32	3	9.1	6	1	UN06_CLOPA	P81351 clostridium
33	2	6.1	4	1	DCMS_PSECH	P19918 pseudomonas
34	2	6.1	5	1	BPP7_BOTIN	P30425 bothrops in
35	2	6.1	6	1	VP19_HSV1K	P23210 herpes simp
36	1	3.0	3	1	THYL_PIG	P01151 sus scrofa
37	1	3.0	5	1	BIOB_CITFR	P12997 citrobacter
38	1	3.0	6	1	TMOF_SARBU	P41495 sarcophaga

ALIGNMENTS

RESULT 1
FARP_MONEX
ID FARP_MONEX STANDARD; PRT; 6 AA.
AC P41966;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE FMRFAMIDE-LIKE NEUROPEPTIDE GNFFRF-AMIDE.
OS Moniezia expansa (Sheep tapeworm).
OC Eukaryota; Metazoa; Platyhelminthes; Neodermata; Cestoda; Eucestoda;
OC Cyclophyllidea; Anoplocephalidae; Moniezia.
RN [1]
RP SEQUENCE.
RX MEDLINE=93312289; PubMed=8323531;
RA Maule A.G., Shaw C., Halton D.W., Thim L.;
RT "GNFFRFamide: a novel FMRFamide-immunoreactive peptide isolated from
RT the sheep tapeworm, Moniezia expansa.";
RL Biochem. Biophys. Res. Commun. 193:1054-1060(1993).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 6 6 AMIDATION.
SQ SEQUENCE 6 AA; 787 MW; 69D409C9C4481000 CRC64;

Query Match 39.4%; Score 13; DB 1; Length 6;
Best Local Similarity 66.7%; Pred. No. 8.9e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GDF 5
|:|
Db 1 GNF 3

RESULT 2
UXA4_CHLTR
ID UXA4_CHLTR STANDARD; PRT; 5 AA.
AC P38005;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE UNKNOWN PROTEIN FROM 2D-PAGE FROM ELEMENTARY BODY (FRAGMENT).
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
RN [1]
RP SEQUENCE.
RC STRAIN=L2/434/BU;
RA Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,
RA Comanducci M., Christianen G., Birkelund S., Vtretou E., Ratti G.,
RA Pallini V.;
RL Submitted (SEP-1994) to the SWISS-PROT data bank.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.5, ITS MW IS: 28 KDA.
FT NON_TER 5 5
SQ SEQUENCE 5 AA; 474 MW; 75BAA865AA800000 CRC64;

Query Match 36.4%; Score 12; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GD 4
||

```
Db      3 GD 4


RESULT   3
UF01_MOUSE
ID   UF01_MOUSE     STANDARD;      PRT;     5 AA.
AC   P38639;
DT   01-OCT-1994 (Rel. 30, Created)
DT   01-OCT-1994 (Rel. 30, Last sequence update)
DT   01-FEB-1995 (Rel. 31, Last annotation update)
DE   UNKNOWN PROTEIN FROM 2D-PAGE OF FIBROBLASTS (P19) (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RP   SEQUENCE.
RC   TISSUE=FIBROBLAST;
RX   MEDLINE=95009907; PubMed=7523103;
RA   Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT   "Separation and sequencing of familiar and novel murine proteins
RT   using preparative two-dimensional gel electrophoresis.";
RL   Electrophoresis 15:735-745(1994).
CC   -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC       PROTEIN IS: 6.6, ITS MW IS: 19 KDA.
FT   NON_TER       5       5
SQ   SEQUENCE   5 AA;  717 MW;  7364087043100000 CRC64;


  Query Match             33.3%;  Score 11;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 8.9e+04;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GR 2
          ||
Db      3 GR 4


RESULT   4
TPIS_CANFA
ID   TPIS_CANFA     STANDARD;      PRT;     5 AA.
AC   P54714;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   TRIOSEPHOSPHATE ISOMERASE (EC 5.3.1.1) (TIM) (FRAGMENT).
GN   TPI1.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
RN   [1]
RP   SEQUENCE.
RC   TISSUE=HEART;
RX   MEDLINE=98163340; PubMed=9504812;
RA   Dunn M.J., Corbett J.M., Wheeler C.H.;
RT   "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT   dog heart proteins.";
RL   Electrophoresis 18:2795-2802(1997).
CC   -!- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE = DIHYDROXY-
CC       ACETONE PHOSPHATE.
CC   -!- PATHWAY: PLAYS AN IMPORTANT ROLE IN SEVERAL METABOLIC PATHWAYS.
CC   -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.
DR   HSC-2DPAGE; P54714; DOG.
DR   INTERPRO; IPR000652; -.
DR   PROSITE; PS00171; TIM; PARTIAL.
KW   Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
KW   Pentose shunt.
FT   NON_TER       1       1
FT   NON_TER       5       5
SQ   SEQUENCE   5 AA;  550 MW;  64444862C9A00000 CRC64;


  Query Match             30.3%;  Score 10;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 8.9e+04;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 FV 6
          ||
Db      1 FV 2


RESULT   5
CIP1_MYTED
ID   CIP1_MYTED     STANDARD;      PRT;     6 AA.
AC   P13736;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   CONTRACTION-INHIBITING PEPTIDE I (MIP I).
OS   Mytilus edulis (Blue mussel).
OC   Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
OC   Mytiloidea; Mytilidae; Mytilus.
RN   [1]
RP   SEQUENCE.
RC   TISSUE=PEDAL GANGLION;
RX   MEDLINE=88240357; PubMed=3377776;
RA   Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;
RT   "Structures and actions of Mytilus inhibitory peptides.";
RL   Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
CC   -!- FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN
CC       MUSCLES.
CC   -!- SIMILARITY: TO MIP II.
DR   PIR; A27696; A27696.
KW   Hormone; Amidation.
FT   MOD_RES       6       6       AMIDATION.
SQ   SEQUENCE   6 AA;  637 MW;  72C9C68775B81000 CRC64;


  Query Match             30.3%;  Score 10;  DB 1;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 8.9e+04;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 FV 6
          ||
Db      5 FV 6


RESULT   6
CIP2_MYTED
ID   CIP2_MYTED     STANDARD;      PRT;     6 AA.
AC   P13737;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   CONTRACTION-INHIBITING PEPTIDE II (MIP II).
OS   Mytilus edulis (Blue mussel).
OC   Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
OC   Mytiloidea; Mytilidae; Mytilus.
RN   [1]
RP   SEQUENCE.
RC   TISSUE=PEDAL GANGLION;
RX   MEDLINE=88240357; PubMed=3377776;
RA   Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;
RT   "Structures and actions of Mytilus inhibitory peptides.";
RL   Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
CC   -!- FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN
CC       MUSCLES.
CC   -!- SIMILARITY: TO MIP I.
DR   PIR; B27696; B27696.
KW   Hormone; Amidation.
FT   MOD_RES       6       6       AMIDATION.
SQ   SEQUENCE   6 AA;  621 MW;  72C9C6876DD81000 CRC64;


  Query Match             30.3%;  Score 10;  DB 1;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 8.9e+04;
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  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 FV 6
          ||
Db      5 FV 6


RESULT   7
ACH1_ACHFU
ID   ACH1_ACHFU     STANDARD;      PRT;     4 AA.
AC   P35904;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   ACHATIN-I.
OS   Achatina fulica (Giant African snail).
OC   Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC   Achatinacea; Achatinidae; Achatina.
RN   [1]
RP   SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.
RC   STRAIN=FERUSSAC; TISSUE=GANGLION;
RX   MEDLINE=89273551; PubMed=2597281;
RA   Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,
RA   Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Li P.,
RA   Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.;
RT   "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina
RT   fulica Ferussac containing a D-amino acid residue.";
RL   Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
RN   [2]
RP   CHARACTERIZATION.
RC   STRAIN=FERUSSAC; TISSUE=HEART ATRIUM;
RX   MEDLINE=91264856; PubMed=1675568;
RA   Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,
RA   Yoshida M., Harada A., Muneoka Y., Kobayashi M.;
RT   "Purification of achatin-I from the atria of the African giant snail,
RT   Achatina fulica, and its possible function.";
RL   Biochem. Biophys. Res. Commun. 177:847-853(1991).
RN   [3]
RP   X-RAY CRYSTALLOGRAPHY.
RX   MEDLINE=93014529; PubMed=1399265;
RA   Ishida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,
RA   Iwashita T., Nomoto K.;
RT   "Crystal structure and molecular conformation of achatin-I
RT   (H-Gly-D-Phe-Ala-Asp-OH), an endogenous neuropeptide containing a
RT   D-amino acid residue.";
RL   Int. J. Pept. Protein Res. 39:258-264(1992).
CC   -!- FUNCTION: NEUROEXCITATORY PEPTIDE; INCREASES THE IMPULSE FREQUENCY
CC       AND PRODUCES A SPIKE BROADENING OF THE IDENTIFIED HEART EXCITATORY
CC       NEURON (PON); ALSO ENHANCES THE AMPLITUDE AND FREQUENCY OF THE
CC       HEART BEAT. HAS ALSO AN EFFECT ON SEVERAL OTHER MUSCLES.
DR   PIR; A32480; A32480.
KW   Hormone; D-amino acid.
FT   MOD_RES       2       2       D-PHENYLALANINE.
SQ   SEQUENCE   4 AA;  408 MW;  6AADD9C810000000 CRC64;


  Query Match          27.3%;  Score 9;  DB 1;  Length 4;
  Best Local Similarity   50.0%;  Pred. No. 8.9e+04;
  Matches    2;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 GRGD 4
          |  |
Db      1 GFAD 4


RESULT   8
PAP2_PARMA
ID   PAP2_PARMA     STANDARD;      PRT;     5 AA.
AC   P81864;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   01-OCT-2000 (Rel. 40, Last annotation update)
DE   PARDAXIN II (PXII) (FRAGMENT).
OS   Pardachirus marmoratus (Red sea moses sole).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC   Soleoidei; Soleidae; Pardachirus.
RN   [1]
RP   SEQUENCE.
RC   TISSUE=SKIN SECRETION;
RX   MEDLINE=87057369; PubMed=3782138;
RA   Lazarovici P., Primor N., Loew L.M.;
RT   "Purification and pore-forming activity of two hydrophobic
RT   polypeptides from the secretion of the Red sea moses sole (Pardachirus
RT   marmoratus).";
RL   J. Biol. Chem. 261:16704-16713(1986).
CC   -!- FUNCTION: EXHIBITS UNUSUAL SHARK REPELLENT AND SURFACTANT
CC       PROPERTIES. FORMS VOLTAGE-DEPENDENT, ION-PERMEABLE CHANNELS
CC       IN MEMBRANES. AT HIGH CONCENTRATION CAUSES CELL MEMBRANE LYSIS.
CC   -!- SUBUNIT: MONOMER. IN AQUEOUS SOLUTION EXISTS AS A TETRAMER.
CC   -!- SUBCELLULAR LOCATION: SECRETED.
CC   -!- SIMILARITY: BELONGS TO THE PARDAXIN FAMILY.
KW   Toxin.
FT   NON_TER       5       5
SQ   SEQUENCE   5 AA;  614 MW;  7769C9C9C8100000 CRC64;


  Query Match          27.3%;  Score 9;  DB 1;  Length 5;
  Best Local Similarity   66.7%;  Pred. No. 8.9e+04;
  Matches    2;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      3 GDF 5
          | |
Db      1 GFF 3


RESULT   9
TRM3_ECOLI
ID   TRM3_ECOLI     STANDARD;      PRT;     5 AA.
AC   P13973;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   TRAM PROTEIN (FRAGMENT).
GN   TRAM.
OS   Escherichia coli.
OG   Plasmid IncFII R100.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Escherichia.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88227859; PubMed=2836369;
RA   Inamoto S., Yoshioka Y., Ohtsubo E.;
RT   "Identification and characterization of the products from the traJ
RT   and traY genes of plasmid R100.";
RL   J. Bacteriol. 170:2749-2757(1988).
CC   -!- FUNCTION: TRANSFER GENE PROTEIN. IS INVOLVED IN THE CONJUGATION
CC       PROCESS OF BACTERIAL CELLS FOR THE EXCHANGE OF PLASMID DNA.
CC   -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC   -!- SIMILARITY: TO TRAM PROTEIN OF OTHER PLASMIDS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M20941; -; NOT_ANNOTATED_CDS.
DR   PIR; A32014; A32014.
KW   Conjugation; Plasmid; DNA-binding.
FT   NON_TER       1       1
SQ   SEQUENCE   5 AA;  634 MW;  6B1B1AA443500000 CRC64;
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  Query Match             24.2%;  Score 8;  DB 1;  Length 5;
  Best Local Similarity   33.3%;  Pred. No. 8.9e+04;
  Matches    1;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 RGD 4
          : |
Db      1 KND 3


RESULT  10
FLRF_HIRME
ID   FLRF_HIRME     STANDARD;      PRT;     4 AA.
AC   P42561;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   01-NOV-1995 (Rel. 32, Last annotation update)
DE   FLRFAMIDE.
OS   Hirudo medicinalis (Medicinal leech), and Helisoma trivolvis (Snail).
OC   Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC   Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
RN   [1]
RP   SEQUENCE.
RC   SPECIES=H.MEDICINALIS;
RX   MEDLINE=92195954; PubMed=1686933;
RA   Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT   "Identification of RFamide neuropeptides in the medicinal leech.";
RL   Peptides 12:897-908(1991).
RN   [2]
RP   SEQUENCE.
RC   SPECIES=H.TRIVOLVIS; TISSUE=KIDNEY;
RX   MEDLINE=94286417; PubMed=7912428;
RA   Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT   "FMRFamide-related peptides from the kidney of the snail, Helisoma
RT   trivolvis.";
RL   Peptides 15:31-36(1994).
CC   -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC       FAMILY.
KW   Neuropeptide; Amidation.
FT   MOD_RES       4      4       AMIDATION.
SQ   SEQUENCE   4 AA;  582 MW;  69D40729A0000000 CRC64;


  Query Match             21.2%;  Score 7;  DB 1;  Length 4;
  Best Local Similarity   50.0%;  Pred. No. 8.9e+04;
  Matches    1;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 FV 6
          |:
Db      1 FL 2


RESULT  11
FMRF_MACNI
ID   FMRF_MACNI     STANDARD;      PRT;     4 AA.
AC   P01162;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   FMRFAMIDE (PEAK C) (CARDIOEXCITATORY NEUROPEPTIDE).
OS   Macrocallista nimbosa (Sun-ray clam), Nereis virens (Sandworm),
OS   Hirudo medicinalis (Medicinal leech), and Helisoma trivolvis (Snail).
OC   Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroida;
OC   Veneroidea; Veneridae; Macrocallista.
RN   [1]
RP   SEQUENCE, AND SYNTHESIS.
RC   SPECIES=M.NIMBOSA; TISSUE=CEREBRAL PEDAL, AND VISCERAL GANGLION;
RX   MEDLINE=77215956; PubMed=877582;
RA   Price D.A., Greenberg M.J.;
RT   "Structure of a molluscan cardioexcitatory neuropeptide.";
RL   Science 197:670-671(1977).
RN   [2]
RP   SEQUENCE, AND CHARACTERIZATION.
RC   SPECIES=M.NIMBOSA; TISSUE=GANGLION;
RX   MEDLINE=78012038; PubMed=909875;
RA   Price D.A., Greenberg M.J.;
RT   "Purification and characterization of a cardioexcitatory neuropeptide
RT   from the central ganglia of a bivalve mollusc.";
RL   Prep. Biochem. 7:261-281(1977).
RN   [3]
RP   SEQUENCE.
RC   SPECIES=N.VIRENS;
RX   MEDLINE=90259866; PubMed=2342992;
RA   Krajniak K.G., Price D.A.;
RT   "Authentic FMRFamide is present in the polychaete Nereis virens.";
RL   Peptides 11:75-77(1990).
RN   [4]
RP   SEQUENCE.
RC   SPECIES=H.MEDICINALIS;
RX   MEDLINE=92195954; PubMed=1686933;
RA   Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT   "Identification of RFamide neuropeptides in the medicinal leech.";
RL   Peptides 12:897-908(1991).
RN   [5]
RP   SEQUENCE.
RC   SPECIES=H.TRIVOLVIS; TISSUE=KIDNEY;
RX   MEDLINE=94286417; PubMed=7912428;
RA   Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT   "FMRFamide-related peptides from the kidney of the snail, Helisoma
RT   trivolvis.";
RL   Peptides 15:31-36(1994).
CC   -!- FUNCTION: MYOACTIVE; CARDIOEXCITATORY SUBSTANCE. PHARMACOLOGICAL
CC       ACTIVITIES INCLUDE AUGMENTATION, INDUCTION, AND REGULARIZATION OF
CC       CARDIAC CONTRACTION.
CC   -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC       FAMILY.
DR   PIR; A01426; ECNK.
DR   PIR; A60418; A60418.
KW   Neuropeptide; Amidation.
FT   MOD_RES       4      4       AMIDATION.
SQ   SEQUENCE   4 AA;  600 MW;  69D40699A0000000 CRC64;


  Query Match             21.2%;  Score 7;  DB 1;  Length 4;
  Best Local Similarity   50.0%;  Pred. No. 8.9e+04;
  Matches    1;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 FV 6
          |:
Db      1 FM 2


RESULT  12
GRWM_HUMAN
ID   GRWM_HUMAN     STANDARD;      PRT;     3 AA.
AC   P01157;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   21-JUL-1986 (Rel. 01, Last annotation update)
DE   GROWTH-MODULATING PEPTIDE.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=77162369; PubMed=858356;
RA   Schlesinger D.H., Pickart L., Thaler M.M.;
RT   "Growth-modulating serum tripeptide is glycyl-histidyl-lysine.";
RL   Experientia 33:324-325(1977).
CC   -!- MISCELLANEOUS: THIS SERUM TRIPEPTIDE HAS BEEN FOUND TO STIMULATE
CC       GROWTH OF SOME CELL TYPES AND TO INHIBIT OTHER TYPES IN VITRO.
DR   PIR; A01421; GKHU.
SQ   SEQUENCE   3 AA;  340 MW;  6331E81000000000 CRC64;


  Query Match             18.2%;  Score 6;  DB 1;  Length 3;
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  Best Local Similarity   100.0%;  Pred. No. 8.9e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 G 1
          |
Db      1 G 1


RESULT  13
LUXE_VIBFI
ID   LUXE_VIBFI     STANDARD;      PRT;     3 AA.
AC   P24272;
DT   01-MAR-1992 (Rel. 21, Created)
DT   01-MAR-1992 (Rel. 21, Last sequence update)
DT   01-OCT-1996 (Rel. 34, Last annotation update)
DE   LONG-CHAIN-FATTY-ACID--LUCIFERIN-COMPONENT LIGASE (EC 6.2.1.19)
DE   (ACYL-PROTEIN SYNTHETASE) (FRAGMENT).
GN   LUXE.
OS   Vibrio fischeri.
OC   Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91072226; PubMed=2254256;
RA   Swartzman E., Kapoor S., Graham A.F., Meighen E.A.;
RT   "A new Vibrio fischeri lux gene precedes a bidirectional termination
RT   site for the lux operon.";
RL   J. Bacteriol. 172:6797-6802(1990).
CC   -!- FUNCTION: ACYL-PROTEIN SYNTHETASE ACTIVATES TETRADECANOIC ACID.
CC       IT IS A COMPONENT OF THE FATTY ACID REDUCTASE COMPLEX RESPONSIBLE
CC       FOR CONVERTING TETRADECANOIC ACID TO THE ALDEHYDE WHICH SERVES AS
CC       SUBSTRATE IN THE LUCIFERASE-CATALYZED REACTION.
CC   -!- CATALYTIC ACTIVITY: ATP + AN ACID + PROTEIN = AMP + PYROPHOSPHATE
CC       + AN ACYL-PROTEIN THIOLESTER.
CC   -!- PATHWAY: SECOND STEP IN THE BIOLUMINESCENT FATTY ACID REDUCTASE
CC       COMPLEX.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M62812; -; NOT_ANNOTATED_CDS.
KW   Luminescence; Ligase.
FT   NON_TER       1       1
SQ   SEQUENCE   3 AA;  374 MW;  6AA3303000000000 CRC64;


  Query Match             18.2%;  Score 6;  DB 1;  Length 3;
  Best Local Similarity   100.0%;  Pred. No. 8.9e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 D 4
          |
Db      3 D 3


RESULT  14
DCML_PSECH
ID   DCML_PSECH     STANDARD;      PRT;     4 AA.
AC   P19916;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   01-DEC-1992 (Rel. 24, Last annotation update)
DE   CARBON MONOXIDE DEHYDROGENASE LARGE CHAIN (EC 1.2.99.2) (FRAGMENT).
OS   Pseudomonas carboxydohydrogena.
OC   Bacteria; Proteobacteria.
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=90055678; PubMed=2818128;
RA   Kraut M., Hugendieck I., Herwig S., Meyer O.;
RT   "Homology and distribution of CO dehydrogenase structural genes in
RT   carboxydotrophic bacteria.";
RL   Arch. Microbiol. 152:335-341(1989).
CC   -!- CATALYTIC ACTIVITY: CO + H(2)O + ACCEPTOR = CO(2) + REDUCED
CC       ACCEPTOR.
CC   -!- COFACTOR: MOLYBDENUM.
CC   -!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
CC       SMALL.
DR   PIR; PL0140; PL0140.
KW   Oxidoreductase; Molybdenum.
FT   NON_TER       4       4
SQ   SEQUENCE   4 AA;  441 MW;  7761E876F0000000 CRC64;


  Query Match             18.2%;  Score 6;  DB 1;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 8.9e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 G 1
          |
Db      2 G 2


RESULT  15
EOSI_HUMAN
ID   EOSI_HUMAN     STANDARD;      PRT;     4 AA.
AC   P02731;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   21-JUL-1986 (Rel. 01, Last annotation update)
DE   EOSINOPHILOTACTIC PEPTIDES.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=76078412; PubMed=1060093;
RA   Goetzl E.J., Austen K.F.;
RT   "Purification and synthesis of eosinophilotactic tetrapeptides of
RT   human lung tissue: identification as eosinophil chemotactic factor of
RT   anaphylaxis.";
RL   Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).
CC   -!- MISCELLANEOUS: THESE PEPTIDES ARE RELEASED FROM MAST CELLS IN LUNG
CC       (AND OTHER TISSUES) DURING HYPERSENSITIVITY REACTIONS
CC       (ANAPHYLAXIS). THEIR ACTIVITIES, PREFERENTIALLY AFFECTING
CC       EOSINOPHILS, INCLUDE CHEMOTAXIS, CHEMOTACTIC DEACTIVATION, RELEASE
CC       OF ENZYMES, AND STIMULATION OF THE HEXOSE MONOPHOSPHATE SHUNT.
DR   PIR; A03190; ETHUL.
FT   VARIANT       1       1       V -> A (IN OTHER PEPTIDE).
FT                                 /FTId=VAR_005201.
SQ   SEQUENCE   4 AA;  390 MW;  6B05B862A0000000 CRC64;


  Query Match             18.2%;  Score 6;  DB 1;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 8.9e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 G 1
          |
Db      2 G 2


Search completed: March  6, 2001, 09:44:29
Job time: 108 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: March 6, 2001, 09:42:22 ; Search time 19.02 Seconds
(without alignments)
36.974 Million cell updates/sec

Title: US-09-081-522-4
Perfect score: 33
Sequence: 1 GRGDFV 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 13

Minimum DB seq length: 0
Maximum DB seq length: 6

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_15:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	12	36.4	5	13	P82070	P82070 litoria rub
2	10	30.3	5	13	P82099	P82099 litoria rub
3	10	30.3	6	13	P82096	P82096 litoria rub
4	9	27.3	5	13	P82073	P82073 litoria rub
5	9	27.3	5	13	P82100	P82100 litoria rub
6	8	24.2	5	13	P82071	P82071 litoria rub
7	8	24.2	5	13	P82072	P82072 litoria rub
8	6	18.2	6	4	Q08720	Q08720 homo sapien
9	5	15.2	6	10	P82181	P82181 spinacia ol
10	5	15.2	6	10	P82182	P82182 spinacia ol
11	5	15.2	6	10	P82541	P82541 spinacia ol
12	4	12.1	4	11	Q08433	Q08433 rattus norv
13	2	6.1	5	10	Q99007	Q99007 hordeum vul

ALIGNMENTS

RESULT 1
P82070
ID P82070 PRELIMINARY; PRT; 5 AA.
AC P82070;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE RUBELLIDIN 1.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=SKIN SECRETION;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australin red tree frog
RT 'Litoria rubella'. the skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
CC -!- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
CC ANTIBIOTIC ACTIVITY.
CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -!- MASS SPECTROMETRY: MW=598; METHOD=FAB.
KW Amphibian skin.
SQ SEQUENCE 5 AA; 598 MW; 6DD9C9CAB2A00000 CRC64;

Query Match 36.4%; Score 12; DB 13; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DF 5
||
Db 2 DF 3

RESULT 2
P82099
ID P82099 PRELIMINARY; PRT; 5 AA.
AC P82099;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE ELECTRIN 3.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=SKIN SECRETION;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litori electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:0-0(1999).
KW Amphibian skin; Amidation.
FT MOD_RES 5 5 AMIDATION.
SQ SEQUENCE 5 AA; 630 MW; 668761F2C9A00000 CRC64;

Query Match 30.3%; Score 10; DB 13; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FV 6
||
Db 1 FV 2

```
RESULT   3
P82096
ID   P82096      PRELIMINARY;      PRT;     6 AA.
AC   P82096;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   ELECTRIN 1.
OS   Litoria rubella (Desert tree frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC   Litoria.
OX   NCBI_TaxID=104895;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=SKIN SECRETION;
RA   Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT   "Peptides from the skin glands of the Australian buzzing tree frog
RT   Litori electrica. Comparison with the skin peptides from Litoria
RT   rubella.";
RL   Aust. J. Chem. 52:0-0(1999).
KW   Amphibian skin; Amidation.
FT   MOD_RES       6       6       AMIDATION.
SQ   SEQUENCE   6 AA;  792 MW;  6683704772C9A000 CRC64;


  Query Match             30.3%;  Score 10;  DB 13;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 FV 6
          ||
Db      1 FV 2


RESULT   4
P82073
ID   P82073      PRELIMINARY;      PRT;     5 AA.
AC   P82073;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   RUBELLIDIN 3.2.
OS   Litoria rubella (Desert tree frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC   Litoria.
OX   NCBI_TaxID=104895;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=SKIN SECRETION;
RA   Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT   "Peptides from the skin glands of the Australian buzzing tree frog
RT   Litori electrica. Comparison with the skin peptides from Litoria
RT   rubella.";
RL   Aust. J. Chem. 52:0-0(1999).
CC   -!- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
CC       ANTIBIOTIC ACTIVITY.
CC   -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
KW   Amphibian skin.
SQ   SEQUENCE   5 AA;  570 MW;  71A9C9C862A00000 CRC64;


  Query Match             27.3%;  Score 9;  DB 13;  Length 5;
  Best Local Similarity   66.7%;  Pred. No. 3.7e+05;
  Matches    2;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      3 GDF 5
          | |
Db      2 GFF 4


RESULT   5
P82100
ID   P82100      PRELIMINARY;      PRT;     5 AA.
AC   P82100;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   ELECTRIN 4.
OS   Litoria rubella (Desert tree frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC   Litoria.
OX   NCBI_TaxID=104895;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=SKIN SECRETION;
RA   Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT   "Peptides from the skin glands of the Australian buzzing tree frog
RT   Litori electrica. Comparison with the skin peptides from Litoria
RT   rubella.";
RL   Aust. J. Chem. 52:0-0(1999).
KW   Amphibian skin; Amidation.
FT   MOD_RES       5       5       AMIDATION.
SQ   SEQUENCE   5 AA;  616 MW;  61F2D1A059A00000 CRC64;


  Query Match             27.3%;  Score 9;  DB 13;  Length 5;
  Best Local Similarity   50.0%;  Pred. No. 3.7e+05;
  Matches    1;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 FV 6
          |:
Db      1 FI 2


RESULT   6
P82071
ID   P82071      PRELIMINARY;      PRT;     5 AA.
AC   P82071;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   RUBELLIDIN 2.1.
OS   Litoria rubella (Desert tree frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC   Litoria.
OX   NCBI_TaxID=104895;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=SKIN SECRETION;
RA   Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA   Tyler M.J., Wallace J.C.;
RT   "The structure of new peptides from the Australin red tree frog
RT   'Litoria rubella'. the skin peptide profile as a probe for the study
RT   of evolutionary trends of amphibians.";
RL   Aust. J. Chem. 49:955-963(1996).
CC   -!- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
CC       ANTIBIOTIC ACTIVITY.
CC   -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC   -!- MASS SPECTROMEIRY: MW=626; METHOD=FAB.
KW   Amphibian skin.
SQ   SEQUENCE   5 AA;  626 MW;  6DD9C9CB10300000 CRC64;


  Query Match             24.2%;  Score 8;  DB 13;  Length 5;
  Best Local Similarity   50.0%;  Pred. No. 3.7e+05;
  Matches    1;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 DF 5
          :|
Db      2 EF 3
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RESULT   7
P82072
ID   P82072      PRELIMINARY;      PRT;     5 AA.
AC   P82072;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   RUBELLIDIN 3.1.
OS   Litoria rubella (Desert tree frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC   Litoria.
OX   NCBI_TaxID=104895;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=SKIN SECRETION;
RA   Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA   Tyler M.J., Wallace J.C.;
RT   "The structure of new peptides from the Australin red tree frog
RT   'Litoria rubella'. the skin peptide profile as a probe for the study
RT   of evolutionary trends of amphibians.";
RL   Aust. J. Chem. 49:955-963(1996).
CC   -!- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
CC       ANTIBIOTIC ACTIVITY.
CC   -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC   -!- MASS SPECTROMETRY: MW=655; METHOD=FAB.
KW   Amphibian skin; Amidation.
FT   MOD_RES       5       5       AMIDATION.
SQ   SEQUENCE   5 AA;  656 MW;  71A9C9CB10300000 CRC64;


  Query Match             24.2%;  Score 8;  DB 13;  Length 5;
  Best Local Similarity   50.0%;  Pred. No. 3.7e+05;
  Matches    1;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 DF 5
          :|
Db      2 EF 3


RESULT   8
Q08720
ID   Q08720      PRELIMINARY;      PRT;     6 AA.
AC   Q08720;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   Y PROTEIN (FRAGMENT).
GN   CREB.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93010691; PubMed=1396344;
RA   Waeber G., Habener J.F.;
RT   "Novel testis germ cell-specific transcript of the CREB gene contains
RT   an alternatively spliced exon with multiple in-frame stop codons.";
RL   Endocrinology 131:2010-2015(1992).
DR   EMBL; X68994; CAA48780.1; -.
FT   NON_TER       1       1
FT   NON_TER       6       6
SQ   SEQUENCE   6 AA;  695 MW;  67272EB9C735D000 CRC64;


  Query Match             18.2%;  Score 6;  DB 4;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 F 5
          |
Db      3 F 3


RESULT   9
P82181
ID   P82181      PRELIMINARY;      PRT;     6 AA.
AC   P82181;
DT   01-JUN-2000 (TrEMBLrel. 14, Created)
DT   01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT   01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE   CHLOROPLAST 50S RIBOSOMAL PROTEIN L10 BETA (FRAGMENT).
OS   Spinacia oleracea (Spinach).
OC   Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC   Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae;
OC   Caryophyllales; Chenopodiaceae; Spinacia.
OX   NCBI_TaxID=3562;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=CV. ALWARO; TISSUE=LEAF;
RA   Yamaguchi K., von Knoblauch K., Subramanian A.R.;
RT   "Identification of all the proteins in the large subunit of an
RT   organelle (chloroplast) ribosome.";
RL   J. Biol. Chem. 0:0-0(2000).
CC   -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
CC   -!- SUBCELLULAR LOCATION: CHLOROPLAST AND OTHER PLASTIDS.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC   -!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
DR   INTERPRO; IPR002363; -.
DR   PROSITE; PS01109; RIBOSOMAL_L10; 1.
KW   Ribosomal protein; Chloroplast; rRNA-binding.
FT   NON_TER       6       6
SQ   SEQUENCE   6 AA;  675 MW;  6321B415B05DB000 CRC64;


  Query Match             15.2%;  Score 5;  DB 10;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 R 2
          |
Db      4 R 4


RESULT  10
P82182
ID   P82182      PRELIMINARY;      PRT;     6 AA.
AC   P82182;
DT   01-JUN-2000 (TrEMBLrel. 14, Created)
DT   01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT   01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE   CHLOROPLAST 50S RIBOSOMAL PROTEIN L10 GAMMA (FRAGMENT).
OS   Spinacia oleracea (Spinach).
OC   Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC   Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae;
OC   Caryophyllales; Chenopodiaceae; Spinacia.
OX   NCBI_TaxID=3562;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=CV. ALWARO; TISSUE=LEAF;
RA   Yamaguchi K., von Knoblauch K., Subramanian A.R.;
RT   "Identification of all the proteins in the large subunit of an
RT   organelle (chloroplast) ribosome.";
RL   J. Biol. Chem. 0:0-0(2000).
CC   -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
CC   -!- SUBCELLULAR LOCATION: CHLOROPLAST AND OTHER PLASTIDS.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC   -!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
DR   INTERPRO; IPR002363; -.
DR   PROSITE; PS01109; RIBOSOMAL_L10; 1.
KW   Ribosomal protein; Chloroplast; rRNA-binding.
FT   NON_TER       6       6
SQ   SEQUENCE   6 AA;  675 MW;  6321B415B05DB000 CRC64;
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  Query Match             15.2%;  Score 5;  DB 10;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 R 2
          |
Db      4 R 4


RESULT  11
P82541
ID   P82541      PRELIMINARY;      PRT;     6 AA.
AC   P82541;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   CHLOROPLAST 30S RIBOSOMAL PROTEIN S19 BETA (FRAGMENT).
OS   Spinacia oleracea (Spinach).
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC   Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae;
OC   Caryophyllales; Chenopodiaceae; Spinacia.
OX   NCBI_TaxID=3562;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=CV. ALWARO;
RA   Yamaguchi K., von Knoblauch K., Subramanian A.R.;
RT   "Identification of all the proteins in the small subunit of an
RT   organelle (chloroplast) ribosome.";
RL   J. Biol. Chem. 0:0-0(2000).
CC   -!- SUBCELLULAR LCCATION: CHLOROPLAST AND OTHER PLASTIDS.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC   -!- MISCELLANEOUS: S19 ALPHA AND BETA FORMS DIFFER IN PI. S19 BETA
CC       FORM IS THE MINOR BASIC FORM.
CC   -!- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
DR   INTERPRO; IPR002222; -.
DR   PROSITE; PS00323; RIBOSOMAL_S19; PARTIAL.
KW   Ribosomal protein; Chloroplast.
FT   NON_TER       6       6
SQ   SEQUENCE   6 AA;  732 MW;  63333735A411C000 CRC64;


  Query Match             15.2%;  Score 5;  DB 10;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 R 2
          |
Db      2 R 2


RESULT  12
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ID   Q08433      PRELIMINARY;      PRT;     4 AA.
AC   Q08433;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
DE   UDP-GLUCURONOSYLTRANSFERASE, MICROSOMAL (EC 2.4.1.17) (UDPGT)
DE   (FRAGMENT).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=GUNN;
RX   MEDLINE=91282758; PubMed=1840486;
RA   Sato H., Aono S., Kashiwamata S., Koiwai O.;
RT   "Genetic defect of bilirubin UDP-glucuronosyltransferase in the
RT   hyperbilirubinemic Gunn rat.";
RL   Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
CC   -!- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
CC       SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
CC       ENDOGENOUS COMPOUNDS.
CC   -!- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
CC       BETA-D-GLUCORONOSIDE.
CC   -!- SUBCELLULAR LOCATION: MICROSOME.
DR   EMBL; S38636; AAB19259.1; -.
KW   Transferase; Glycosyltransferase; Microsome; Multigene family.
FT   NON_TER       1       1
FT   NON_TER       4       4
SQ   SEQUENCE   4 AA;  473 MW;  633732C420000000 CRC64;


  Query Match             12.1%;  Score 4;  DB 11;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      6 V 6
          |
Db      2 V 2


RESULT  13
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ID   Q99007      PRELIMINARY;      PRT;     5 AA.
AC   Q99007;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   ALPHA-AMYLASE (EC 3.2.1.1) (FRAGMENT).
GN   AMY1.
OS   Hordeum vulgare (Barley).
OC   Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC   Magnoliophyta; Liliopsida; Poales; Poaceae; Hordeum.
OX   NCBI_TaxID=4513;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=HIMALAYA; TISSUE=ALEURONE LAYER;
RX   MEDLINE=91329704; PubMed=1831055;
RA   Jacobsen J.V., Close T.J.;
RT   "Control of transient expression of chimaeric genes by gibberellic
RT   acid and abscisic acid in protoplasts prepared from mature barley
RT   aleurone layers.";
RL   Plant Mol. Biol. 16:713-721(1991).
CC   -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC
CC       LINKAGES IN OLIGOSACCHARIDES AND POLYASACCHARIDES.
CC   -!- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC   -!- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN
CC       BARLEY.
DR   EMBL; X54643; CAA38455.1; -.
KW   Hydrolase; Glycosidase; Carbohydrate metabolism; Seed; Germination;
KW   Calcium; Multigene family.
FT   NON_TER       5       5
SQ   SEQUENCE   5 AA;  600 MW;  61E3344DD6F00000 CRC64;


  Query Match              6.1%;  Score 2;  DB 10;  Length 5;
  Best Local Similarity    0.0%;  Pred. No. 3.7e+05;
  Matches    0;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 R 2
          :
Db      4 K 4


Search completed: March  6, 2001, 09:43:34
Job time: 72 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: March 6, 2001, 09:44:54 ; Search time 30.08 Seconds
(without alignments)
5.684 Million cell updates/sec

Title: US-09-081-522-5
Perfect score: 27
Sequence: 1 RGDFV 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 14863

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	27	100.0	5	15	R45382	Cell adhesion inhi
2	27	100.0	5	15	R45384	Cell adhesion inhi
3	27	100.0	5	15	R45386	Cell adhesion inhi
4	27	100.0	5	15	R45387	Cell adhesion inhi
5	27	100.0	5	16	R82387	Cyclic integrin al
6	27	100.0	5	16	R82389	Cyclic integrin al
7	27	100.0	5	18	W33057	Alpha-v, beta-5 vi
8	27	100.0	5	18	W33055	Alpha-v, beta-5 vi
9	27	100.0	5	19	W41099	Alpha-v beta-3 ant
10	27	100.0	5	19	W41101	Alpha-v beta-3 ant
11	27	100.0	5	19	W41109	Alpha-v beta-3 ant
12	27	100.0	5	19	W41240	Alpha-v-beta-5 ant
13	27	100.0	5	19	W41243	Alpha-v-beta-5 ant
14	27	100.0	5	19	W41247	Alpha-v-beta-5 ant
15	27	100.0	5	20	W92307	Cyclic azapeptide
16	24	88.9	5	20	W92302	Cyclic adhesion in
17	24	88.9	5	20	W92306	Cyclic adhesion in
18	23	85.2	4	12	R10408	Fibrinogen recepto
19	23	85.2	4	13	R25316	Cell contact inhib
20	23	85.2	4	14	R32386	Fibrinogen recepto
21	23	85.2	4	14	R69333	Gp IIb/IIIa recept
22	23	85.2	4	15	R54528	Platelet aggregati
23	23	85.2	4	15	R49800	Sequence of peptid
24	23	85.2	4	15	R42568	Tri-/tetra-cyclic
25	23	85.2	4	18	W25179	RGD-peptide capabl
26	23	85.2	4	19	W52096	Targetting peptide
27	23	85.2	4	19	W50599	GPIIb/IIIa recepto
28	23	85.2	5	12	R10179	RGD-contg. peptide
29	23	85.2	5	12	R11760	Peptide #4 having
30	23	85.2	5	13	R24515	Platelet antagonis
31	23	85.2	5	18	Y08052	Biotin derivative
32	23	85.2	5	18	Y08055	Biotin derivative
33	23	85.2	5	18	W35358	Cyclic integrin an
34	23	85.2	5	18	W35359	Cyclic integrin an
35	23	85.2	5	18	W35355	Cyclic integrin an
36	23	85.2	5	18	W35356	Cyclic integrin an
37	23	85.2	5	18	W35357	Cyclic integrin an
38	23	85.2	5	18	W35353	Cyclic integrin an
39	23	85.2	5	18	W35354	Cyclic integrin an
40	23	85.2	5	18	W35352	Cyclic integrin an
41	23	85.2	5	18	W13156	Integrin inhibitin
42	23	85.2	5	18	W13160	Integrin inhibitin
43	23	85.2	5	19	W41110	Cyclic peptide 112
44	23	85.2	5	19	W41246	Alpha-v-beta-5 ant
45	23	85.2	5	20	Y43231	RGD-containing pep

ALIGNMENTS

RESULT 1
R45382
ID R45382 standard; Protein; 5 AA.
XX
AC R45382;
XX
DT 06-JUL-1994 (first entry)
XX
DE Cell adhesion inhibition peptide (m).
XX
KW Cyclopentapeptide; cyclohexapeptide; inhibition; adhesion;
KW animal; somatic; cell; thrombosis; myocardial infarction;
KW apoplexy; arteriosclerosis; inflammation; angina pectoris;
KW osteoporosis; tumour; adhesion-receptor antagonist; osteoclast;
KW wound healing; beta-3 integrin; fibrogen binding.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "D-form residue, Amide linkage to Val5 forming
FT a cyclic peptide"
FT Modified-site 5
FT /note= "Amide linkage to Arg1 forming a cyclic peptide"
XX
PN EP579083-A.
XX
PD 12-JAN-1994.
XX
PF 26-JUN-1993; 93EP-0110232.
XX
PR 06-JUL-1992; 92US-0909367.
PR 24-FEB-1993; 93US-0022024.
XX
PA (MERE) MERCK PATENT GMBH.

```
XX
PI   Cheresh DA,  Diefenbach B,  Felding-Habermann B,  Gurrath M;
PI   Hoelzemann G,  Jonczyk A,  Kessler H,  Melzer G,  Mueller G;
XX
DR   WPI; 1994-009982/02.
XX
PT   Compsn. contg. cyclopenta- or hexa-peptide - inhibits adhesion of
PT   animal cells, used in the treatment and prophylaxis of e.g.
PT   thrombosis, tumours, osteoporosis or inflammation
XX
PS   Claim 1; Page 7; 9pp; English.
XX
CC   The sequences given in R45370-87 are cyclopenta- and
CC   cyclohexapeptides which act to inhibit adhesion between animal cells.
CC   A composition containing these peptides may be used in the
CC   treatment and prophylaxis of thrombosis, myocardial infarction,
CC   apoplexy, arteriosclerosis, inflammation, angina pectoris,
CC   osteoporosis and/or tumour.  They are used to induce an adhesion-
CC   receptor antagonist effect in the subject, to inhibit cell adhesion,
CC   and in the formation of osteoclasts.  They may also be used in wound
CC   healing compositions and to block beta-3 integrin fibrogen binding.
XX
SQ   Sequence   5 AA;


  Query Match             100.0%;  Score 27;  DB 15;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RGDFV 5
          |||||
Db      1 rgdfv 5


RESULT   2
R45384
ID   R45384 standard; Protein; 5 AA.
XX
AC   R45384;
XX
DT   06-JUL-1994  (first entry)
XX
DE   Cell adhesion inhibition peptide (o).
XX
KW   Cyclopentapeptide; cyclohexapeptide; inhibition; adhesion;
KW   animal; somatic; cell; thrombosis; myocardial infarction;
KW   apoplexy; arteriosclerosis; inflammation; angina pectoris;
KW   osteoporosis; tumour; adhesion-receptor antagonist; osteoclast;
KW   wound healing; beta-3 integrin; fibrogen binding.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1
FT                   /note= "Amide linkage to Val5 forming a cyclic peptide"
FT   Misc-difference 4
FT                   /note= "D-form residue"
FT   Modified-site   5
FT                   /note= "Amide linkage to Arg1 forming a cyclic peptide"
XX
PN   EP578083-A.
XX
PD   12-JAN-1994.
XX
PF   26-JUN-1993;   93EP-0110232.
XX
PR   06-JUL-1992;   92US-0909367.
PR   24-FEB-1993;   93US-0022024.
XX
PA   (MERE ) MERCK PATENT GMBH.
XX
PI   Cheresh DA,  Diefenbach B,  Felding-Habermann B,  Gurrath M;
PI   Hoelzemann G,  Jonczyk A,  Kessler H,  Melzer G,  Mueller G;
XX
DR   WPI; 1994-009982/02.
XX
PT   Compsn. contg. cyclopenta- or hexa-peptide - inhibits adhesion of
PT   animal cells, used in the treatment and prophylaxis of e.g.
PT   thrombosis, tumours, osteoporosis or inflammation
XX
PS   Claim 1; Page 7; 9pp; English.
XX
CC   The sequences given in R45370-87 are cyclopenta- and
CC   cyclohexapeptides which act to inhibit adhesion between animal cells.
CC   A composition containing these peptides may be used in the
CC   treatment and prophylaxis of thrombosis, myocardial infarction,
CC   apoplexy, arteriosclerosis, inflammation, angina pectoris,
CC   osteoporosis and/or tumour.  They are used to induce an adhesion-
CC   receptor antagonist effect in the subject, to inhibit cell adhesion,
CC   and in the formation of osteoclasts.  They may also be used in wound
CC   healing compositions and to block beta-3 integrin fibrogen binding.
XX
SQ   Sequence   5 AA;


  Query Match             100.0%;  Score 27;  DB 15;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RGDFV 5
          |||||
Db      1 rgdfv 5


RESULT   3
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ID   R45386 standard; Protein; 5 AA.
XX
AC   R45386;
XX
DT   06-JUL-1994  (first entry)
XX
DE   Cell adhesion inhibition peptide (q).
XX
KW   Cyclopentapeptide; cyclohexapeptide; inhibition; adhesion;
KW   animal; somatic; cell; thrombosis; myocardial infarction;
KW   apoplexy; arteriosclerosis; inflammation; angina pectoris;
KW   osteoporosis; tumour; adhesion-receptor antagonist; osteoclast;
KW   wound healing; beta-3 integrin; fibrogen binding.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1
FT                   /note= "Amide linkage to Val5 forming a cyclic peptide"
FT   Modified-site   5
FT                   /note= "D-form residue, Amide linkage to Arg1 forming
FT                          a cyclic peptide"
XX
PN   EP578083-A.
XX
PD   12-JAN-1994.
XX
PF   26-JUN-1993;   93EP-0110232.
XX
PR   06-JUL-1992;   92US-0909367.
PR   24-FEB-1993;   93US-0022024.
XX
PA   (MERE ) MERCK PATENT GMBH.
XX
PI   Cheresh DA,  Diefenbach B,  Felding-Habermann B,  Gurrath M;
PI   Hoelzemann G,  Jonczyk A,  Kessler H,  Melzer G,  Mueller G;
XX
DR   WPI; 1994-009982/02.
XX
PT   Compsn. contg. cyclopenta- or hexa-peptide - inhibits adhesion of
```

```
PT   animal cells, used in the treatment and prophylaxis of e.g.
PT   thrombosis, tumours, osteoporosis or inflammation
XX
PS   Claim 1; Page 7; 9pp; English.
XX
CC   The sequences given in R45370-87 are cyclopenta- and
CC   cyclohexapeptides which act to inhibit adhesion between animal cells.
CC   A composition containing these peptides may be used in the
CC   treatment and prophylaxis of thrombosis, myocardial infarction,
CC   apoplexy, arteriosclerosis, inflammation, angina pectoris,
CC   osteoporosis and/or tumour.  They are used to induce an adhesion-
CC   receptor antagonist effect in the subject, to inhibit cell adhesion,
CC   and in the formation of osteoclasts.  They may also be used in wound
CC   healing compositions and to block beta-3 integrin fibrogen binding.
XX
SQ   Sequence   5 AA;


  Query Match             100.0%;  Score 27;  DB 15;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RGDFV 5
          |||||
Db      1 rgdfv 5


RESULT   4
R45387
ID   R45387 standard; Protein; 5 AA.
XX
AC   R45387;
XX
DT   06-JUL-1994  (first entry)
XX
DE   Cell adhesion inhibition peptide (r).
XX
KW   Cyclopentapeptide; cyclohexapeptide; inhibition; adhesion;
KW   animal; somatic; cell; thrombosis; myocardial infarction;
KW   apoplexy; arteriosclerosis; inflammation; angina pectoris;
KW   osteoporosis; tumour; adhesion-receptor antagonist; osteoclast;
KW   wound healing; beta-3 integrin; fibrogen binding.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1
FT                   /note= "Amide linkage to Val5 forming a cyclic peptide"
FT   Misc-difference 3
FT                   /note= "D-form residue"
FT   Modified-site   5
FT                   /note= "Amide linkage to Arg1 forming a cyclic peptide"
XX
PN   EP578083-A.
XX
PD   12-JAN-1994.
XX
PF   26-JUN-1993;   93EP-0110232.
XX
PR   06-JUL-1992;   92US-0909367.
PR   24-FEB-1993;   93US-0022024.
XX
PA   (MERE ) MERCK PATENT GMBH.
XX
PI   Cheresh DA,  Diefenbach B,  Felding-Habermann B,  Gurrath M;
PI   Hoelzemann G,  Jonczyk A,  Kessler H,  Melzer G,  Mueller G;
XX
DR   WPI; 1994-009982/02.
XX
PT   Compsn. contg. cyclopenta- or hexa-peptide - inhibits adhesion of
PT   animal cells, used in the treatment and prophylaxis of e.g.
PT   thrombosis, tumours, osteoporosis or inflammation
XX
PS   Claim 1; Page 7; 9pp; English.
XX
CC   The sequences given in R45370-87 are cyclopenta- and
CC   cyclohexapeptides which act to inhibit adhesion between animal cells.
CC   A composition containing these peptides may be used in the
CC   treatment and prophylaxis of thrombosis, myocardial infarction,
CC   apoplexy, arteriosclerosis, inflammation, angina pectoris,
CC   osteoporosis and/or tumour.  They are used to induce an adhesion-
CC   receptor antagonist effect in the subject, to inhibit cell adhesion,
CC   and in the formation of osteoclasts.  They may also be used in wound
CC   healing compositions and to block beta-3 integrin fibrogen binding.
XX
SQ   Sequence   5 AA;


  Query Match             100.0%;  Score 27;  DB 15;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RGDFV 5
          |||||
Db      1 rgdfv 5


RESULT   5
R82387
ID   R82387 standard; peptide; 5 AA.
XX
AC   R82387;
XX
DT   03-MAY-1996  (first entry)
XX
DE   Cyclic integrin alpha-v-beta-3 inhibitor peptide no. 62184.
XX
KW   Integrin; alpha-v-beta-3; inhibitor; angiogenesis; antagonist;
KW   fibrinogen; inflammation; apoptosis; restenosis; cyclic.
XX
OS   Synthetic.
XX
PN   WO9525543-A1.
XX
PD   28-SEP-1995.
XX
PF   09-MAR-1995;   95WO-US03035.
XX
PR   30-DEC-1994;   94US-0366665.
PR   18-MAR-1994;   94US-0210715.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Brooks P,  Cheresh DA;
XX
DR   WPI; 1995-344463/44.
XX
PT   Inhibition of angiogenesis in a tissue, e.g. following angioplasty
PT   - by admin. of a compsn. comprising an alpha-v-beta3 antagonist,
PT   useful for regression of established tumours, treating inflamed
PT   tissue, etc.
XX
PS   Claim 4; Page 47; 135pp; English.
XX
CC   R82386-96 are a group of inhibitor peptides of integrin alpha-v-beta-3.
CC   The inhibitor peptides may be  administered in a compsn. and are useful
CC   for inhibition of inflamed tissue angiogenesis, e.g. that associated
CC   with rheumatoid arthritis, retinal angiogenesis associated with
CC   diabetic retinopathy, that associated with haemangioma, solid
CC   tumours, or solid tumour metastases. The alpha-v-beta-3 atagonists
CC   are also useful to induce apoptosis in neovasculature in a tissue.
CC   The inhibitor peptides are pref. cyclic and contain an RGD sequence.
XX
SQ   Sequence   5 AA;
```

```
  Query Match           100.0%;  Score 27;  DB 16;  Length 5;
  Best Local Similarity  100.0%;  Pred. No. 2.1e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RGDFV 5
          |||||
Db      1 rgdfv 5


RESULT   6
R82389
ID   R82389 standard; peptide; 5 AA.
XX
AC   R82389;
XX
DT   03-MAY-1996  (first entry)
XX
DE   Cyclic integrin alpha-v-beta-3 inhibitor peptide no. 62187.
XX
KW   Integrin; alpha-v-beta-3; inhibitor; angiogenesis; antagonist;
KW   fibrinogen; inflammation; apoptosis; restenosis; cyclic.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 4
FT                   /note= "D-Val"
XX
PN   WO9525543-A1.
XX
PD   28-SEP-1995.
XX
PF   09-MAR-1995;   95WO-US03035.
XX
PR   30-DEC-1994;   94US-0366665.
PR   18-MAR-1994;   94US-0210715.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Brooks P,  Cheresh DA;
XX
DR   WPI; 1995-344463/44.
XX
PT   Inhibition of angiogenesis in a tissue, e.g. following angioplasty
PT   - by admin. of a compsn. comprising an alpha-v-beta3 antagonist,
PT   useful for regression of established tumours, treating inflamed
PT   tissue, etc.
XX
PS   Claim 4; Page 47; 135pp; English.
XX
CC   R82386-96 are a group of inhibitor peptides of integrin alpha-v-beta-3.
CC   The inhibitor peptides may be  administered in a compsn. and are useful
CC   for inhibition of inflamed tissue angiogenesis, e.g. that associated
CC   with rheumatoid arthritis, retinal angiogenesis associated with
CC   diabetic retinopathy, that associated with haemangioma, solid
CC   tumours, or solid tumour metastases. The alpha-v-beta-3 atagonists
CC   are also useful to induce apoptosis in neovasculature in a tissue.
CC   The inhibitor peptides are pref. cyclic and contain an RGD sequence.
XX
SQ   Sequence   5 AA;


  Query Match           100.0%;  Score 27;  DB 16;  Length 5;
  Best Local Similarity  100.0%;  Pred. No. 2.1e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RGDFV 5
          |||||
Db      1 rgdfv 5


RESULT   7
W33057
ID   W33057 standard; peptide; 5 AA.
XX
AC   W33057;
XX
DT   26-JAN-1998  (first entry)
XX
DE   Alpha-v, beta-5 vitronectin receptor antagonist.
XX
KW   RGD containing peptide; antagonist; alpha-v, beta-5;
KW   vitronectin receptor; inhibition; angiogenesis; inflammation;
KW   rheumatoid arthritis; eye disease; diabetic retinopathy;
KW   age related macular degeneration; ocular histoplasmosis;
KW   retinopathy; prematurity; neovascular glaucoma;
KW   corneal neovascular disorder; transplantation; herpetic; luetic;
KW   keratitis; pterygium; neovascular pannus; haemangioma;
KW   solid tumour; metastasis; cytokine; low toxicity;
KW   vascular endothelial growth factor;
KW   transforming growth factor alpha; epidermal growth factor; cyclic.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 5
FT                   /note= "D-form residue"
XX
PN   WO9706791-A1.
XX
PD   27-FEB-1997.
XX
PF   13-AUG-1996;   96WO-US13194.
XX
PR   14-AUG-1995;   95US-0514799.
PR   14-AUG-1996;   96ZA-0006886.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Brooks P,  Cheresh DA,  Friedlander M;
XX
DR   WPI; 1997-165019/15.
XX
PT   Inhibiting angiogenesis with an antagonist selective for the
PT   alpha-v,beta-5 integrin receptor - e.g. antibody, RGD peptide or
PT   organic mimetic, for treatment of inflammation, eye disease, tumours
PT   etc.
XX
PS   Claim 5; Page 105; 126pp; English.
XX
CC   The present RGD containing peptide is an antagonist of the alpha-v,
CC   beta-5 vitronectin receptor, which can be used to inhibit
CC   angiogenesis in alpha-v, beta-5 containing tissue, specifically
CC   angiogenesis as a result of inflammation (especially rheumatoid
CC   arthritis), eye disease (especially diabetic retinopathy, age
CC   related macular degeneration, ocular histoplasmosis, retinopathy of
CC   prematurity or neovascular glaucoma), corneal neovascular disorders
CC   (especially transplantation, herpetic or luetic keratitis,
CC   pterygium and neovascular pannus associated with wearing contact
CC   lenses), haemangioma, solid tumours and their metastases or
CC   cytokines (especially vascular endothelial growth factor,
CC   transforming growth factor alpha or epidermal growth factor). The
CC   antagonist has the advantage of being very specific, affecting no
CC   processes other than angiogenesis and therefore of relatively low
CC   toxicity.
XX
SQ   Sequence   5 AA;


  Query Match           100.0%;  Score 27;  DB 18;  Length 5;
  Best Local Similarity  100.0%;  Pred. No. 2.1e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RGDFV 5
          |||||
Db      1 rgdfv 5
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RESULT   8
W33055
ID   W33055 standard; peptide; 5 AA.
XX
AC   W33055;
XX
DT   26-JAN-1998  (first entry)
XX
DE   Alpha-v, beta-5 vitronectin receptor antagonist.
XX
KW   RGD containing peptide; antagonist; alpha-v, beta-5;
KW   vitronectin receptor; inhibition; angiogenesis; inflammation;
KW   rheumatoid arthritis; eye disease; diabetic retinopathy;
KW   age related macular degeneration; ocular histoplasmosis;
KW   retinopathy; prematurity; neovascular glaucoma;
KW   corneal neovascular disorder; transplantation; herpetic; luetic;
KW   keratitis; pterygium; neovascular pannus; haemangioma;
KW   solid tumour; metastasis; cytokine; low toxicity;
KW   vascular endothelial growth factor;
KW   transforming growth factor alpha; epidermal growth factor; cyclic.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 4
FT                   /note= "D-form residue"
XX
PN   WO9706791-A1.
XX
PD   27-FEB-1997.
XX
PF   13-AUG-1996;   96WO-US13194.
XX
PR   14-AUG-1995;   95US-0514799.
PR   14-AUG-1996;   96ZA-0006886.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Brooks P,  Cheresh DA,  Friedlander M;
XX
DR   WPI; 1997-165019/15.
XX
PT   Inhibiting angiogenesis with an antagonist selective for the
PT   alpha-v,beta-5 integrin receptor - e.g. antibody, RGD peptide or
PT   organic mimetic, for treatment of inflammation, eye disease, tumours
PT   etc.
XX
PS   Claim 5; Page 105; 126pp; English.
XX
CC   The present RGD containing peptide is an antagonist of the alpha-v,
CC   beta-5 vitronectin receptor, which can be used to inhibit
CC   angiogenesis in alpha-v, beta-5 containing tissue, speicfically
CC   angiogenesis as a result of inflammation (especially rheumatoid
CC   arthritis), eye disease (especially diabetic retinopathy, age
CC   related macular degeneration, ocular histoplasmosis, retinopathy of
CC   prematurity or neovascular glaucoma), corneal neovascular disorders
CC   (especially transplantation, herpetic or luetic keratitis,
CC   pterygium and neovascular pannus associated with wearing contact
CC   lenses), haemangioma, solid tumours and their metastases or
CC   cytokines (especially vascular endothelial growth factor,
CC   transforming growth factor alpha or epidermal growth factor). The
CC   antagonist has the advantage of being very specific, affecting no
CC   processes other than angiogenesis and therefore of relatively low
CC   toxicity.
XX
SQ   Sequence   5 AA;

  Query Match             100.0%;  Score 27;  DB 18;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RGDFV 5
           |||||
Db       1 rgdfv 5


RESULT   9
W41099
ID   W41099 standard; Peptide; 5 AA.
XX
AC   W41099;
XX
DT   08-JUN-1998  (first entry)
XX
DE   Alpha-v beta-3 antagonist cyclic peptide 62184 (66203).
XX
KW   Angiogenesis: inhibitor; antagonist; integrin alpha-v beta-3;
KW   vitronectin receptor; rheumatoid arthritis; tumour; metastasis;
KW   diabetic retinopathy; macular degeneration; restenosis; therapy;
KW   circular; cyclic.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 4
FT                   /note= "D-form residue"
XX
PN   WO9745137-A1.
XX
PD   04-DEC-1997.
XX
PF   30-MAY-1997;   97WO-US09158.
XX
PR   31-MAY-1996;   96US-0018733.
PR   31-MAY-1996;   96US-0015869.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Brooks P,  Cheresh DA;
XX
DR   WPI; 1998-032334/03.
XX
PT   Packaging material containing polypeptide antagonist of alphav,
PT   beta3 integrin - used for inhibition of angiogenesis, and for
PT   treating tumours, inflammation, eye diseases etc.
XX
PS   Example 1; Page 48; 234pp; English.
XX
CC   This synthetic RGD-containing cyclic peptide, designated 62184 or
CC   66203, is a particularly preferred peptide that has integrin
CC   alpha-v beta-3 antagonist activity.  It exhibits preferential
CC   inhibition of fibrinogen binding to the alpha-v beta-3 receptor.
CC   It can be prepared using standard solid-phase synthesis
CC   techniques.  The invention relates to the discovery that
CC   angiogenesis is mediated by the specific vitronectin receptor
CC   alpha-v beta-3, and that inhibition of alpha-v beta-3 function
CC   inhibits angiogenesis.  Claimed antagonists of alpha-v beta-3
CC   comprise C-terminal fragments (see W41083-94) of human or chicken
CC   matrix metalloproteinase-2, fusion polypeptides, cyclic or linear
CC   polypeptides, derivatised polypeptides, a monoclonal antibody or
CC   organic mimetic compound.  They can be used to inhibit angiogenesis
CC   in inflammed tissue (for treatment of arthritis or rheumatoid
CC   arthritis), in solid tumours or metastases (particularly to induce
CC   regression or inhibit tumour growth), and in ocular disorders such
CC   as diabetic retinopathy and macular degeneration, as well as to
CC   treat restenosis (all claimed).
XX
SQ   Sequence   5 AA;

  Query Match             100.0%;  Score 27;  DB 19;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy      1 RGDFV 5
          |||||
Db      1 rgdfv 5


RESULT  10
W41101
ID   W41101 standard; Peptide; 5 AA.
XX
AC   W41101;
XX
DT   08-JUN-1998  (first entry)
XX
DE   Alpha-v beta-3 antagonist cyclic peptide 62187.
XX
KW   Angiogenesis; inhibitor; antagonist; integrin alpha-v beta-3;
KW   vitronectin receptor; rheumatoid arthritis; tumour; metastasis;
KW   diabetic retinopathy; macular degeneration; restenosis; therapy;
KW   circular; cyclic.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 5
FT                   /note= "D-form residue"
XX
PN   WO9745137-A1.
XX
PD   04-DEC-1997.
XX
PF   30-MAY-1997;    97WO-US09158.
XX
PR   31-MAY-1996;    96US-0018733.
PR   31-MAY-1996;    96US-0015869.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Brooks P,  Cheresh DA;
XX
DR   WPI; 1998-032334/03.
XX
PT   Packaging material containing polypeptide antagonist of alphav,
PT   beta3 integrin - used for inhibition of angiogenesis, and for
PT   treating tumours, inflammation, eye diseases etc.
XX
PS   Example 1; Page 48; 234pp; English.
XX
CC   This synthetic RGD-containing cyclic peptide, designated 62187,
CC   is a particularly preferred peptide that has integrin
CC   alpha-v beta-3 antagonist activity.  It exhibits preferential
CC   inhibition of fibrinogen binding to the alpha-v beta-3 receptor.
CC   It can be prepared using standard solid-phase synthesis
CC   techniques.  The invention relates to the discovery that
CC   angiogenesis is mediated by the specific vitronectin receptor
CC   alpha-v beta-3, and that inhibition of alpha-v beta-3 function
CC   inhibits angiogenesis.  Claimed antagonists of alpha-v beta-3
CC   comprise C-terminal fragments (see W41083-94) of human or chicken
CC   matrix metalloproteinase-2, fusion polypeptides, cyclic or linear
CC   polypeptides, derivatised polypeptides, a monoclonal antibody or
CC   organic mimetic compound.  They can be used to inhibit angiogenesis
CC   in inflammed tissue (for treatment of arthritis or rheumatoid
CC   arthritis), in solid tumours or metastases (particularly to induce
CC   regression or inhibit tumour growth), and in ocular disorders such
CC   as diabetic retinopathy and macular degeneration, as well as to
CC   treat restenosis (all claimed).
XX
SQ   Sequence   5 AA;


  Query Match             100.0%;  Score 27;  DB 19;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

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Qy      1 RGDFV 5
          |||||
Db      1 rgdfv 5


RESULT  11
W41109
ID   W41109 standard; Peptide; 5 AA.
XX
AC   W41109;
XX
DT   08-JUN-1998  (first entry)
XX
DE   Alpha-v beta-3 antagonist cyclic peptide 121974 (85189).
XX
KW   Angiogenesis; inhibitor; antagonist; integrin alpha-v beta-3;
KW   vitronectin receptor; rheumatoid arthritis; tumour; metastasis;
KW   diabetic retinopathy; macular degeneration; restenosis; therapy;
KW   circular; cyclic.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   5
FT                   /note= "valine residue NH2 terminal is
FT                   methylated"
XX
PN   WO9745137-A1.
XX
PD   04-DEC-1997.
XX
PF   30-MAY-1997;    97WO-US09158.
XX
PR   31-MAY-1996;    96US-0018733.
PR   31-MAY-1996;    96US-0015869.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Brooks P,  Cheresh DA;
XX
DR   WPI; 1998-032334/03.
XX
PT   Packaging material containing polypeptide antagonist of alphav,
PT   beta3 integrin - used for inhibition of angiogenesis, and for
PT   treating tumours, inflammation, eye diseases etc.
XX
PS   Example 1; Page 51; 234pp; English.
XX
CC   This synthetic RGD-containing cyclic peptide, designated 121974 or
CC   85189, is a particularly preferred peptide that has integrin
CC   alpha-v beta-3 antagonist activity.  It can be prepared using
CC   standard solid-phase synthesis techniques.  The invention relates
CC   to the discovery that angiogenesis is mediated by the specific
CC   vitronectin receptor alpha-v beta-3, and that inhibition of alpha-v
CC   beta-3 function inhibits angiogenesis.  Claimed antagonists of
CC   alpha-v beta-3 comprise C-terminal fragments (see W41083-94) of
CC   human or chicken matrix metalloproteinase-2, fusion polypeptides,
CC   cyclic or linear polypeptides, derivatised polypeptides, a
CC   monoclonal antibody or organic mimetic compound.  They can be used
CC   to inhibit angiogenesis in inflammed tissue (for treatment of
CC   arthritis or rheumatoid arthritis), in solid tumours or metastases
CC   (particularly to induce regression or inhibit tumour growth), and
CC   in ocular disorders such as diabetic retinopathy and macular
CC   degeneration, as well as to treat restenosis (all claimed).
XX
SQ   Sequence   5 AA;


  Query Match             100.0%;  Score 27;  DB 19;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy      1 RGDFV 5
          |||||
Db      1 rgdfv 5


RESULT  12
W41240
ID   W41240 standard; protein; 5 AA.
XX
AC   W41240;
XX
DT   09-JUN-1998  (first entry)
XX
DE   Alpha-v-beta-5 antagonistic peptide 62184.
XX
KW   Alpha-v-beta-5 antagonist; treatment; vitronectin receptor; inhibition;
KW   angiogenesis; tumour growth; restenosis; neovascularisation.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1..5
FT                   /note= "peptide is made cyclic via the first and
FT                    last residues"
FT   Misc-difference 4
FT                   /note= "D-form residue"
XX
PN   WO9745447-A1.
XX
PD   04-DEC-1997.
XX
PF   30-MAY-1997;   97WO-US09099.
XX
PR   31-MAY-1996;   96US-0018733.
PR   31-MAY-1996;   96US-0015869.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Brooks P,  Cheresh DA,  Friedlander M;
XX
DR   WPI; 1998-041758/04.
XX
PT   Packaging material containing polypeptide antagonist of alphav,
PT   beta5 integrin - used for inhibition of angiogenesis, and for
PT   treating tumours, inflammation, eye diseases etc.
XX
PS   Disclosure; Page 41; 117pp; English.
XX
CC   The present peptide represents an alpha-v-beta-5 integrin antagonists.
CC   Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of alpha-v-beta-5
CC   can inhibit angiogenesis. The specification describes a novel
CC   labelled package that contains an inhibitor of angiogenesis i.e. an
CC   alpha-v-beta-5 antagonising polypeptide that binds to integrin
CC   alpha-v-beta-5 and includes a part of the C-terminal domain of MMP-2.
CC   The antagonists are used to inhibit angiogenesis in inflamed tissue, in
CC   solid tumours or metastases, and in a wide range of ocular disorders
CC   (e.g. diabetic or other forms of retinopathy, neovascular glaucoma, or
CC   corneal transplants). They are particularly used to induce regression or
CC   to inhibit growth of tumours. The alpha-v-beta-5 antagonists can also be
CC   used to treat restenosis caused by migration of smooth muscle cells
CC   following angioplasty and to reduce blood supply to selected tissues.
CC   The antagonists particularly inhibit neovascularisation where this is
CC   induced by cytokines, e.g. transforming growth factor alpha, epidermal
CC   growth factor or especially vascular endothelial growth factor.
CC   note: this sequence does not appear in the specification; it was created
CC   using information provided.
XX
SQ   Sequence   5 AA;

  Query Match             100.0%;  Score 27;  DB 19;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RGDFV 5
          |||||
Db      1 rgdfv 5


RESULT  13
W41243
ID   W41243 standard; protein; 5 AA.
XX
AC   W41243;
XX
DT   09-JUN-1998  (first entry)
XX
DE   Alpha-v-beta-5 antagonistic peptide 62187.
XX
KW   Alpha-v-beta-5 antagonist; treatment; vitronectin receptor; inhibition;
KW   angiogenesis; tumour growth; restenosis; neovascularisation.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1..5
FT                   /note= "peptide is made cyclic via the first and
FT                    last residues"
FT   Misc-difference 5
FT                   /note= "D-form residue"
XX
PN   WO9745447-A1.
XX
PD   04-DEC-1997.
XX
PF   30-MAY-1997;   97WO-US09099.
XX
PR   31-MAY-1996;   96US-0018733.
PR   31-MAY-1996;   96US-0015869.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Brooks P,  Cheresh DA,  Friedlander M;
XX
DR   WPI; 1998-041753/04.
XX
PT   Packaging material containing polypeptide antagonist of alphav,
PT   beta5 integrin - used for inhibition of angiogenesis, and for
PT   treating tumours, inflammation, eye diseases etc.
XX
PS   Disclosure; Page 41; 117pp; English.
XX
CC   The present peptide represents an alpha-v-beta-5 integrin antagonists.
CC   Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of alpha-v-beta-5
CC   can inhibit angiogenesis. The specification describes a novel
CC   labelled package that contains an inhibitor of angiogenesis i.e. an
CC   alpha-v-beta-5 antagonising polypeptide that binds to integrin
CC   alpha-v-beta-5 and includes a part of the C-terminal domain of MMP-2.
CC   The antagonists are used to inhibit angiogenesis in inflamed tissue, in
CC   solid tumours or metastases, and in a wide range of ocular disorders
CC   (e.g. diabetic or other forms of retinopathy, neovascular glaucoma, or
CC   corneal transplants). They are particularly used to induce regression or
CC   to inhibit growth of tumours. The alpha-v-beta-5 antagonists can also be
CC   used to treat restenosis caused by migration of smooth muscle cells
CC   following angioplasty and to reduce blood supply to selected tissues.
CC   The antagonists particularly inhibit neovascularisation where this is
CC   induced by cytokines, e.g. transforming growth factor alpha, epidermal
CC   growth factor or especially vascular endothelial growth factor.
CC   note: this sequence does not appear in the specification; it was created
CC   using information provided.
XX
SQ   Sequence   5 AA;

  Query Match             100.0%;  Score 27;  DB 19;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+05;
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Db      1 rgdfv 5


RESULT  14
W41247
ID   W41247 standard; protein; 5 AA.
XX
AC   W41247;
XX
DT   09-JUN-1998  (first entry)
XX
DE   Alpha-v-beta-5 antagonistic peptide.
XX
KW   Alpha-v-beta-5 antagonist; treatment; vitronectin receptor; inhibition;
KW   angiogenesis; tumour growth; restenosis; neovascularisation.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 4
FT                   /note= "D-form residue"
XX
PN   WO9745447-A1.
XX
PD   04-DEC-1997.
XX
PF   30-MAY-1997;   97WO-US09099.
XX
PR   31-MAY-1996;   96US-0018733.
PR   31-MAY-1996;   96US-0015869.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Brooks P,  Cheresh DA,  Friedlander M;
XX
DR   WPI; 1998-041758/04.
XX
PT   Packaging material containing polypeptide antagonist of alphav,
PT   beta5 integrin - used for inhibition of angiogenesis, and for
PT   treating tumours, inflammation, eye diseases etc.
XX
PS   Disclosure; Page 38; 117pp; English.
XX
CC   The present peptide represents an alpha-v-beta-5 integrin antagonists.
CC   Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of alpha-v-beta-5
CC   can inhibit angiogenesis. The specification describes a novel
CC   labelled package that contains an inhibitor of angiogenesis i.e. an
CC   alpha-v-beta-5 antagonising polypeptide that binds to integrin
CC   alpha-v-beta-5 and includes a part of the C-terminal domain of MMP-2.
CC   The antagonists are used to inhibit angiogenesis in inflamed tissue, in
CC   solid tumours or metastases, and in a wide range of ocular disorders
CC   (e.g. diabetic or other forms of retinopathy, neovascular glaucoma, or
CC   corneal transplants). They are particularly used to induce regression or
CC   to inhibit growth of tumours. The alpha-v-beta-5 antagonists can also be
CC   used to treat restenosis caused by migration of smooth muscle cells
CC   following angioplasty and to reduce blood supply to selected tissues.
CC   The antagonists particularly inhibit neovascularisation where this is
CC   induced by cytokines, e.g. transforming growth factor alpha, epidermal
CC   growth factor or especially vascular endothelial growth factor.
CC   note: this sequence does not appear in the specification; it was created
CC   using information provided.
XX
SQ   Sequence   5 AA;


  Query Match             100.0%;  Score 27;  DB 19;  Length 5;
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Qy      1 RGDFV 5
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Db      1 rgdfv 5


RESULT  15
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ID   W92307 standard; peptide; 5 AA.
XX
AC   W92307;
XX
DT   01-APR-1999  (first entry)
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DE   Cyclic azapeptide #1.
XX
KW   Cyclic peptide; azapeptide; integrin inhibitor; treatment; thrombosis;
KW   cardiac infarct; coronary heart disease; arteriosclerosis; tumour;
KW   osteoporosis; inflammation; infection; angiogenesis; antimicrobial;
KW   diagnosis; platelet metabolism; fibrinogen receptor; cancer; metastasis;
KW   intracellular signalling; GpIIb/IIIa receptor; matrix metalloproteinase;
KW   vitronectin receptor.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1..5
FT                   /note= "The carboxy group of Val(5) is condensed onto
FT                           the amino group of Arg(1) to form a cyclic
FT                           peptide. Not true N- and C- terminus.
FT                           Val(5) can be modified by N-Me"
FT   Modified-site   2
FT                   /note= "aza-Gly"
FT   Misc-difference 4
FT                   /note= "can be D-form residue"
FT   Misc-difference 5
FT                   /note= "can be D-form residue"
XX
PN   DE19728524-A1.
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PD   07-JAN-1999.
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PF   04-JUL-1997;   97DE-1028524.
XX
PR   04-JUL-1997;   97DE-1028524.
XX
PA   (MERE ) MERCK PATENT GMBH.
XX
PI   Goodman SL,  Jonczyk A,  Kessler H,  Schmitt J,  Wermuth J;
XX
DR   WPI; 1999-072017/07.
XX
PT   New cyclic penta:peptide(s) containing aza-amino acid - are
PT   inhibitors of integrin-ligand interaction, used to treat e.g.
PT   thrombosis, cardiac infarct, coronary heart disease and tumours
XX
PS   Claim 3a; Page 11; 12pp; German.
XX
CC   This invention is concerned with novel cyclic peptides of formula
CC   cyclo(aArg-aGly-aAsp-aX-aY) where aArg = Arg or aza-Arg, aGly = Gly or
CC   aza-Gly, aAsp = Asp or aza-Asp, aX, aY = Ala, Asn, Asp, Arg, Cys, Gln,
CC   Glu, Gly, His, Ile, Leu, Lys, Met, Nle (norleucine), Orn (ornithine),
CC   Phe, Phg (phenylglycine), Pro, Ser, Thr, Tic (tetrahydroisoquinoline-
CC   3-carboxylic acid), Trp, Tyr, Val or NH-Q-CO, or the corresponding
CC   aza-amino acids, Q = 1-6C alkylene, at least one amino acid (aa) in the
CC   peptide has the alpha-carbon atom replaced by nitrogen also the aa may
CC   be derivatised and are coupled together by peptide bonds and optically
CC   active amino acids may be in D- or L-forms. The peptides are integrin
CC   inhibitors, specifically for treating and preventing thrombosis, cardiac
CC   infarct, coronary heart disease, arteriosclerosis, tumours, osteoporosis,
CC   inflammation and infections, or generally any disease where angiogenesis
CC   is involved, in human or veterinary medicine. The peptides also have
CC   antimicrobial activity, are used for diagnosis and location of thrombi,
CC   and for studying metabolism of platelets at different stages of
```

CC activation or intracellular signalling mechanisms of the fibrinogen
CC receptor, and for affinity purification of integrins. The peptides
CC inhibit interaction between the alpha v, beta 3 and beta 5 receptors with
CC their ligands, e.g. they prevent binding of fibrinogen to the GpIIb/IIIa
CC receptor, thus preventing metastatic spread of cancers, and prevent
CC binding of matrix metalloproteinase to the vitronectin (alpha v beta 3)
CC receptor. This sequence is a specific claimed example of a novel peptide
CC of the invention.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 27; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGDFV 5
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Db 1 rgdfv 5

Search completed: March 6, 2001, 09:45:52
Job time: 58 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: March 6, 2001, 09:44:53 ; Search time 19.1 Seconds
(without alignments)
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Title: US-09-081-522-5
Perfect score: 27
Sequence: 1 RGDFV 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 14061

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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5: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	27	100.0	5	1	US-08-210-715-7	Sequence 7, Appli
3	27	100.0	5	1	US-08-366-665-5	Sequence 5, Appli
4	27	100.0	5	1	US-08-366-665-7	Sequence 7, Appli
5	27	100.0	5	2	US-08-616-770-2	Sequence 2, Appli
6	23	85.2	4	1	US-07-932-200-10	Sequence 10, Appl
7	23	85.2	4	1	US-08-596-116A-68	Sequence 68, Appl
8	23	85.2	4	2	US-08-668-871-12	Sequence 12, Appl
9	23	85.2	4	2	US-08-669-683-12	Sequence 12, Appl
10	23	85.2	4	2	US-08-387-749-10	Sequence 10, Appl
11	23	85.2	4	2	US-08-335-832-25	Sequence 25, Appl
12	23	85.2	4	2	US-08-753-781-20	Sequence 20, Appl
13	23	85.2	4	2	US-08-361-864-28	Sequence 28, Appl
14	23	85.2	4	4	PCT-US93-08231-10	Sequence 10, Appl
15	23	85.2	4	5	5330911-12	Patent No. 5330911
16	23	85.2	5	1	US-08-315-026B-10	Sequence 10, Appl
17	23	85.2	5	2	US-08-616-770-1	Sequence 1, Appli
18	23	85.2	5	2	US-08-754-773B-10	Sequence 10, Appl
19	23	85.2	5	3	US-09-141-127-23	Sequence 23, Appl
20	23	85.2	5	3	US-09-155-721-1	Sequence 1, Appli
21	23	85.2	5	3	US-09-155-721-2	Sequence 2, Appli
22	23	85.2	5	3	US-09-155-721-4	Sequence 4, Appli
23	23	85.2	5	3	US-09-155-721-5	Sequence 5, Appli
24	23	85.2	5	3	US-09-155-721-6	Sequence 6, Appli
25	23	85.2	5	3	US-09-155-721-7	Sequence 7, Appli
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28	23	85.2	5	5	5330911-13	Patent No. 5330911
29	22	81.5	5	3	US-08-694-387A-22	Sequence 22, Appl
30	22	81.5	5	3	US-08-694-387A-23	Sequence 23, Appl
31	22	81.5	5	3	US-08-694-387A-24	Sequence 24, Appl
32	22	81.5	5	3	US-08-694-387A-25	Sequence 25, Appl
33	22	81.5	5	3	US-08-694-387A-27	Sequence 27, Appl
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35	22	81.5	5	3	US-08-694-387A-30	Sequence 30, Appl
36	22	81.5	5	3	US-08-694-387A-32	Sequence 32, Appl
37	22	81.5	5	3	US-08-694-387A-33	Sequence 33, Appl
38	22	81.5	5	3	US-08-694-387A-34	Sequence 34, Appl
39	22	81.5	5	3	US-08-694-387A-35	Sequence 35, Appl
40	22	81.5	5	3	US-08-694-387A-37	Sequence 37, Appl
41	22	81.5	5	3	US-08-694-387A-38	Sequence 38, Appl
42	22	81.5	5	3	US-08-694-387A-39	Sequence 39, Appl
43	22	81.5	5	3	US-08-594-387A-40	Sequence 40, Appl
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45	21	77.8	5	1	US-08-210-715-9	Sequence 9, Appli

ALIGNMENTS

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RESULT 1
US-08-210-715-5
; Sequence 5, Application US/08210715
; Patent No. 5753230
; GENERAL INFORMATION:
;   APPLICANT: Brooks, Peter
;   APPLICANT: Cheresh, David A
;   TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR
;   TITLE OF INVENTION: INHIBITION OF ANGIOGENESIS
;   NUMBER OF SEQUENCES: 14
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Office of Patent Counsel, The Scripps
;     ADDRESSEE: Research Institute
;     STREET: 10665 No. 5753230th Torrey Pines Road, TPC-8
;     CITY: La Jolla
;     STATE: CA
;     COUNTRY: USA
;     ZIP: 92037
;   COMPUTER READABLE FORM:
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;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/210,715
;     FILING DATE: 18-MAR-1994
;     CLASSIFICATION: 514
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Fitting, Thomas
;     REGISTRATION NUMBER: 34,163
;     REFERENCE/DOCKET NUMBER: TSRI 419.0
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (619) 554-2937
;     TELEFAX: (619) 554-6312
; INFORMATION FOR SEQ ID NO: 5:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 5 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: circular
;   MOLECULE TYPE: peptide
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   FRAGMENT TYPE: internal
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;     NAME/KEY: Peptide
;     LOCATION: 1..5
;     OTHER INFORMATION: /label= cyclo
;     OTHER INFORMATION: /note= "Cyclo signifies a cyclic peptide; lower
;     OTHER INFORMATION: case letters indicate a D-amino acid; capital
;     OTHER INFORMATION: letters indicate a L-amino acid."
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US-08-210-715-5

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Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGDFV 5
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Db 1 RGDFV 5

RESULT 2
US-08-210-715-7
; Sequence 7, Application US/08210715
; Patent No. 5753230
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheresh, David A
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR
; TITLE OF INVENTION: INHIBITION OF ANGIOGENESIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 No. 5753230th Torrey Pines Road, TPC-8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/210,715
; FILING DATE: 18-MAR-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 419.0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 554-2937
; TELEFAX: (619) 554-6312
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
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; OTHER INFORMATION: /note= "Cyclo signifies a cyclic peptide; lower
; OTHER INFORMATION: case letters indicate a D-amino acid; capital
; OTHER INFORMATION: letters indicate a L-amino acid."
US-08-210-715-7

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Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 RGDFV 5

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; Patent No. 5766591
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheresh, David A
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR
; TITLE OF INVENTION: INHIBITION OF ANGIOGENESIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 No. 5766591th Torrey Pines Road, TPC-8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; APPLICATION NUMBER: US/08/366,665
; FILING DATE: 30-DEC-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/210,715
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 419.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 554-2937
; TELEFAX: (619) 554-6312
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
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; OTHER INFORMATION: case letters indicate a D-amino acid; capital
; OTHER INFORMATION: letters indicate a L-amino acid."
US-08-366-665-5

Query Match 100.0%; Score 27; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGDFV 5
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Db 1 RGDFV 5

RESULT 4
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; Patent No. 5766591
; GENERAL INFORMATION:

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;    APPLICANT:  Brooks, Peter
;    APPLICANT:  Cheresh, David A
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS USEFUL FOR
;    TITLE OF INVENTION:  INHIBITION OF ANGIOGENESIS
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Office of Patent Counsel, The Scripps
;      ADDRESSEE:  Research Institute
;      STREET:  10666 No. 5766591th Torrey Pines Road, TPC-8
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
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;      OPERATING SYSTEM:  PC-DOS/MS-DOS
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;      CLASSIFICATION:  424
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;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fitting, Thomas
;      REGISTRATION NUMBER:  34,163
;      REFERENCE/DOCKET NUMBER:  TSRI 419.1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 554-2937
;      TELEFAX:  (619) 554-6312
;  INFORMATION FOR SEQ ID NO:  7:
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;      LENGTH:  5 amino acids
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US-08-366-665-7


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Db      1 RGDFV 5


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; Patent No. 5849692
;  GENERAL INFORMATION:
;    APPLICANT:  Jonczyk, Alfred
;    APPLICANT:  Holzemann, Gunter
;    APPLICANT:  Felding-Habermann, Brunhilde
;    APPLICANT:  Rippmann, Friedrich
;    APPLICANT:  Diefenbach, Beate
;    APPLICANT:  Kessler, Horst
;    APPLICANT:  Haubner, Roland
;    APPLICANT:  Wermuth, Jochen
;    TITLE OF INVENTION:  Cyclic Peptides Containing Arg-Gly-Asp, and
;    TITLE OF INVENTION:  Derivatives Thereof, as Adhesion Inhibitors
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Millen, White, Zelano & Branigan, P.C.
;      STREET:  2200 Clarendon Boulevard, Suite 1400
;      CITY:  Arlington
;      STATE:  VA
;      COUNTRY:  U.S.A.
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/616,770
;      FILING DATE:  15-MAR-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/220,858
;      FILING DATE:  31-MAR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DE P 43 10 643.9
;      FILING DATE:  01-APR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Heaney, Brion P.
;      REGISTRATION NUMBER:  32,542
;      REFERENCE/DOCKET NUMBER:  MERCK 1566C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-243-6333
;      TELEFAX:  703-243-6410
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US-08-616-770-2


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Qy      1 RGDFV 5
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Db      1 RGDFV 5


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; Patent No. 5366862
;  GENERAL INFORMATION:
;    APPLICANT:  VENTON, DUANE L.
;    APPLICANT:  HOPFINGER, ANTON J.
;    APPLICANT:  LE BRETON, GUY
;    TITLE OF INVENTION:  METHOD FOR GENERATING AND SCREENING
;    TITLE OF INVENTION:  USEFUL PEPTIDES
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 SEVENTH STREET, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
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;      OPERATING SYSTEM:  PC-DOS/MS-DOS
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;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/932,200
;      FILING DATE:  21-AUG-1992
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  COOPER, IVER P.
;      REGISTRATION NUMBER:  28,005
;      REFERENCE/DOCKET NUMBER:  VENTON-1B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;      TELEX:  248633
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-07-932-200-10


  Query Match             85.2%;  Score 23;  DB 1;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RGDF 4
          ||||
Db      1 RGDF 4


RESULT   7
US-08-596-116A-68
; Sequence 68, Application US/08596116A
; Patent No. 5721213
;  GENERAL INFORMATION:
;    APPLICANT:  SATO, Yoshimi
;    APPLICANT:  HAYASHI, Yoshio
;    APPLICANT:  KATADA, Jun
;    TITLE OF INVENTION:  No. 5721213el Peptides, Active as Inhibitors of
;    TITLE OF INVENTION:  Platelet Aggregation
;    NUMBER OF SEQUENCES:  71
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Kenyon & Kenyon
;      STREET:  1025 Connecticut Avenue, N.W., Suite 600
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3+ Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS 6.2
;      SOFTWARE:  WordPerfect 6.1 for Windows
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/596,116A
;      FILING DATE:  30 JAN 1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP94/01611
;      FILING DATE:  29 SEP 1994
;      APPLICATION NUMBER:  JP 245541
;      FILING DATE:  30 SEP 1993
;      APPLICATION NUMBER:  JP 50602
;      FILING DATE:  22 MAR 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Toffenetti, Judith L.
;      REGISTRATION NUMBER:  39,048
;      REFERENCE/DOCKET NUMBER:  2002/3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-429-1776
;      TELEFAX:  202-429-0796
;  INFORMATION FOR SEQ ID NO:  68:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-596-116A-68


  Query Match             85.2%;  Score 23;  DB 1;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RGDF 4
          ||||
Db      1 RGDF 4


RESULT   8
US-08-668-871-12
; Sequence 12, Application US/08668871
; Patent No. 5811389
;  GENERAL INFORMATION:
;    APPLICANT:  Bannwarth, Wilhelm
;    APPLICANT:  Gerber, Fernand
;    APPLICANT:  Grieder, Alfred
;    APPLICANT:  Knierzinger, Andreas
;    APPLICANT:  Mueller, Klaus
;    APPLICANT:  Obrecht, Daniel
;    APPLICANT:  Trzeciak, Arnold
;    TITLE OF INVENTION:  TRI- AND TETRACYCLIC COMPOUNDS
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  United States of America
;      ZIP:  07110-1199
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/668,871
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/105,508
;      FILING DATE:
;      APPLICATION NUMBER:  CH 2725/92
;      FILING DATE:  31-AUG-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kass, Alan P
;      REGISTRATION NUMBER:  32142
;      REFERENCE/DOCKET NUMBER:  RAN 4781/1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 235-4205
;      TELEFAX:  (201) 235-3500
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-668-871-12


  Query Match             85.2%;  Score 23;  DB 2;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy      1 RGDF 4
          ||||
Db      1 RGDF 4


RESULT   9
US-08-669-683-12
; Sequence 12, Application US/08669683
; Patent No. 5811548
;  GENERAL INFORMATION:
;    APPLICANT:  Bannwarth, Wilhelm
;    APPLICANT:  Gerber, Fernand
;    APPLICANT:  Grieder, Alfred
;    APPLICANT:  Knierzinger, Andreas
;    APPLICANT:  Mueller, Klaus
;    APPLICANT:  Obrecht, Daniel
;    APPLICANT:  Trzeciak, Arnold
;    TITLE OF INVENTION:  TRI- AND TETRACYCLIC COMPOUNDS
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  United States of America
;      ZIP:  07110-1199
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/669,683
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/106,508
;      FILING DATE:
;      APPLICATION NUMBER:  CH 2725/92
;      FILING DATE:  31-AUG-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kass, Alan P
;      REGISTRATION NUMBER:  32142
;      REFERENCE/DOCKET NUMBER:  RAN 4781/1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 235-4205
;      TELEFAX:  (201) 235-3500
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-669-683-12


  Query Match           85.2%;  Score 23;  DB 2;  Length 4;
  Best Local Similarity  100.0%;  Pred. No. 1.3e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RGDF 4
          ||||
Db      1 RGDF 4


RESULT  10
US-08-387-749-10
; Sequence 10, Application US/08387749
; Patent No. 5814460
;  GENERAL INFORMATION:
;    APPLICANT:  VENTON, DUANE L.
;    APPLICANT:  HOPFINGER, ANTON J.
;    APPLICANT:  LE BRETON, GUY
;    TITLE OF INVENTION:  METHOD FOR GENERATING AND SCREENING
;    TITLE OF INVENTION:  USEFUL PEPTIDES
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 SEVENTH STREET, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/387,749
;      FILING DATE:  21-Feb-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/08231
;      FILING DATE:  09-AUG-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/932,200
;      FILING DATE:  21-AUG-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/813,315
;      FILING DATE:  21-AUG-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US91/00891
;      FILING DATE:  14-FEB-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/480,865
;      FILING DATE:  14-FEB-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  COOPER, IVER P.
;      REGISTRATION NUMBER:  28,005
;      REFERENCE/DOCKET NUMBER:  VENTON-1C
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;      TELEX:  248633
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-387-749-10


  Query Match           85.2%;  Score 23;  DB 2;  Length 4;
  Best Local Similarity  100.0%;  Pred. No. 1.3e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RGDF 4
          ||||
Db      1 RGDF 4


RESULT  11
US-08-335-832-25
; Sequence 25, Application US/08335832
; Patent No. 5925331
;  GENERAL INFORMATION:
;    APPLICANT:  Dean, Richard T
;    APPLICANT:  Lister-James, John
;    TITLE OF INVENTION:  Technetium-99m Labeled Peptides for
;    TITLE OF INVENTION:  Thrombus Imaging
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
```

```
;       ADDRESSEE:  Banner & Allegretti, Ltd.
;       STREET:  10 South Wacker Drive Suite 3000
;       CITY:  Chicago
;       STATE:  Illinois
;       COUNTRY:  USA
;       ZIP:  60606
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/335,832
;       FILING DATE:  05-JAN-1995
;       CLASSIFICATION:  424
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  No. 5925331nan, Kevin E
;       REGISTRATION NUMBER:  35,303
;       REFERENCE/DOCKET NUMBER:  92,216-I
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  312-715-1000
;       TELEFAX:  312-715-1234
;       TELEX:  910-221-5317
;   INFORMATION FOR SEQ ID NO:  25:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  4 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  1
;       OTHER INFORMATION:  /label= ma
;       OTHER INFORMATION:  /note= "The amino terminus is modified by covalent
;       OTHER INFORMATION:  linkage to an mercaptoacetyl group."
US-08-335-832-25


  Query Match             85.2%;  Score 23;  DB 2;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RGDF 4
          ||||
Db      1 RGDF 4


RESULT  12
US-08-753-781-20
; Sequence 20, Application US/08753781C
; Patent No. 5951981
; GENERAL INFORMATION:
;  APPLICANT: Markland Jr., Francis S.
;  APPLICANT: Bush, Larry R.
;  APPLICANT: Swenson, Stephen
;  APPLICANT: Flores Sanchez, Eladio
;  TITLE OF INVENTION: THROMBOLYTIC AGENTS WITH ANTITHROMBOTIC ACTIVITY
;  FILE REFERENCE: DITI 124
;  CURRENT APPLICATION NUMBER: US/08/753,781C
;  CURRENT FILING DATE: 1996-12-02
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
;   LENGTH: 4
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (1)
;   OTHER INFORMATION: meercaptoacetyl
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:synthetic
;   OTHER INFORMATION: peptide
US-08-753-781-20


  Query Match             85.2%;  Score 23;  DB 2;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RGDF 4
          ||||
Db      1 RGDF 4


RESULT  13
US-08-361-864-28
; Sequence 28, Application US/08361864
; Patent No. 5977064
; GENERAL INFORMATION:
;   APPLICANT:  Dean, Richard T
;   APPLICANT:  Lister-James, John
;   TITLE OF INVENTION:  Multimeric Polyvalent Antithrombotic
;   TITLE OF INVENTION:  Agents
;   NUMBER OF SEQUENCES:  37
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Allegretti & Witcoff, Ltd.
;     STREET:  10 South Wacker Drive, Suite 3000
;     CITY:  Chicago
;     STATE:  Illinois
;     COUNTRY:  USA
;     ZIP:  60606
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/361,864
;     FILING DATE:
;     CLASSIFICATION:  514
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US/07/955,466A
;     FILING DATE:  19921002
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  No. 5977064nan, Kevin E
;     REGISTRATION NUMBER:  35,303
;     REFERENCE/DOCKET NUMBER:  92,668
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  312-715-1000
;     TELEFAX:  312-715-1234
;     TELEX:  910-221-5317
;  INFORMATION FOR SEQ ID NO:  28:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  4 amino acids
;     TYPE:  amino acid
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  peptide
US-08-361-864-28


  Query Match             85.2%;  Score 23;  DB 2;  Length 4;
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  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RGDF 4
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Db      1 RGDF 4


RESULT  14
PCT-US93-08231-10
; Sequence 10, Application PC/TUS9308231
;  GENERAL INFORMATION:
;    APPLICANT:  VENTON, DUANE L.
;    APPLICANT:  HOFFINGER, ANTON J.
```

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;    APPLICANT:  LE BRETON, GUY
;    TITLE OF INVENTION:  METHOD FOR GENERATING AND SCREENING
;    TITLE OF INVENTION:  USEFUL PEPTIDES
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 SEVENTH STREET, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/08231
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  COOPER, IVER P.
;      REGISTRATION NUMBER:  28,005
;      REFERENCE/DOCKET NUMBER:  VENTON1C.PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;      TELEX:  248633
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
PCT-US93-08231-10


  Query Match             85.2%;  Score 23;  DB 4;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RGDF 4
          ||||
Db      1 RGDF 4


RESULT  15
5330911-12
;Patent No. 5330911
;    APPLICANT: HUBBELL, JEFFREY A.;MASSIA, STEPHEN P.;DESAI,
;NEIL P.
;    TITLE OF INVENTION: SURFACES HAVING DESIRABLE CELL
;ADHESIVE EFFECTS
;    NUMBER OF SEQUENCES: 27
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/527,198
;      FILING DATE: 21-MAY-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 414,144
;      FILING DATE: 28-SEP-1989
;SEQ ID NO:12:
;      LENGTH: 4
5330911-12


  Query Match             85.2%;  Score 23;  DB 5;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RGDF 4
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Db      1 RGDF 4
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Search completed: March 6, 2001, 09:45:18
Job time: 25 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: March 6, 2001, 09:44:54 ; Search time 20.46 Seconds
(without alignments)
16.594 Million cell updates/sec

Title: US-09-081-522-5
Perfect score: 27
Sequence: 1 RGDFV 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 205

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_66:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	12	44.4	4	2	PT0711	T-cell receptor be
2	12	44.4	5	2	A32516	cholecystokinin-5
3	12	44.4	5	2	PQ0689	photosystem I 10.4
4	12	44.4	5	2	A44692	fulicin - giant Af
5	12	44.4	5	2	B61445	Leu-enkephalin - b
6	12	44.4	5	2	A61445	Met-enkephalin - b
7	12	44.4	5	2	PT0513	T-cell receptor be
8	12	44.4	5	2	PT0538	T-cell receptor be
9	12	44.4	5	2	PT0703	T-cell receptor be
10	12	44.4	5	2	PT0690	T-cell receptor be
11	12	44.4	5	2	PT0573	T-cell receptor be
12	12	44.4	5	2	PT0679	T-cell receptor be
13	11	40.7	4	1	ECXAA	antho-RFamide neur
14	11	40.7	4	2	A25844	autho-RF amide neu
15	11	40.7	4	2	S39390	myosin-light-chain
16	11	40.7	4	2	S47552	ubiquitin - rat
17	11	40.7	5	2	B61168	cocoonase (EC 3.4.
18	11	40.7	5	2	PT0525	T-cell receptor be
19	11	40.7	5	2	PT0608	T-cell receptor be
20	11	40.7	5	2	PT0695	T-cell receptor be
21	11	40.7	5	2	PT0700	T-cell receptor be
22	9	33.3	5	2	S68326	blood cell protein
23	9	33.3	5	4	A58728	serrawettin W2 - S
24	8	29.6	4	2	D41654	hypothetical prote
25	8	29.6	4	2	PT0677	T-cell receptor be
26	8	29.6	5	2	A32014	traM protein - Esc
27	8	29.6	5	2	B45525	actin I - malaria
28	8	29.6	5	2	PT0540	T-cell receptor be
29	7	25.9	3	2	A23751	spinal cord peptid
30	7	25.9	4	2	ECNK	cardioexcitatory n
31	7	25.9	4	2	S09478	globulin IV alpha
32	7	25.9	4	2	A35779	neuropeptide Antho
33	7	25.9	4	2	A60418	FMRFamide - polych
34	7	25.9	4	2	B53284	T-cell receptor be
35	7	25.9	5	2	PT0308	Ig heavy chain CRD
36	7	25.9	5	2	PT0729	T-cell receptor be
37	6	22.2	3	2	GKHU	growth-modulating
38	6	22.2	3	2	A60898	bursin - chicken
39	6	22.2	3	2	B23751	spinal cord peptid
40	6	22.2	3	2	PT0636	T-cell receptor be
41	6	22.2	3	2	PT0571	T-cell receptor be
42	6	22.2	3	2	S68328	blood cell protein
43	6	22.2	4	2	A32039	tyrosine-melanocyt
44	6	22.2	4	2	PL0140	carbon-monoxide de
45	6	22.2	4	2	A26209	protein-glutamine

ALIGNMENTS

RESULT 1
PT0711
T-cell receptor beta chain V-D-J region (120-2J) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0607; PT0674; PT0678; PT0570; PT0711; PT0710
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A;Reference number: PT0509; MUID:91277601
A;Accession: PT0607
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-4 <FE1>
A;Experimental source: newborn thymus, strain BALB/c, 120-2J
A;Accession: PT0674
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-4 <FE2>
A;Experimental source: day 18 fetal thymus, strain BALB/c, 140-1G
A;Accession: PT0678
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-4 <FE3>
A;Experimental source: day 18 fetal thymus, strain BALB/c, 154-1L
A;Accession: PT0570
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-4 <FE4>
A;Experimental source: day 19 fetal thymus, strain BALB/c, 141-1I
A;Accession: PT0711
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-4 <FE5>
A;Experimental source: newborn thymus, strain BALB/c (clones 161-2AE and 161-2AF)
C;Keywords: T-cell receptor

Query Match 44.4%; Score 12; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      2 GD 3
          ||
Db      3 GD 4
```

RESULT 2
A32516
cholecystokinin-5 - dog
N;Alternate names: CCK-5
C;Species: Canis lupus familiaris (dog)

```
C;Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 18-Aug-2000
C;Accession: A32516
R;Shively, J.; Reeve Jr., J.R.; Eysselein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, J.H.
Am. J. Physiol. 252, G272-G275, 1987
A;Title: CCK-5: sequence analysis of a small cholecystokinin from canine brain and intes
A;Reference number: A32516; MUID:87153871
A;Accession: A32516
A;Molecule type: protein
A;Residues: 1-5 <SHI>
C;Comment: This peptide corresponds to the five carboxyl-terminal residues of cholecysto
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; neuropeptide
F;5/Modified site: amidated carboxyl end (Phe) #status experimental


  Query Match             44.4%;  Score 12;  DB 2;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 2e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 DF 4
           ||
Db       4 DF 5


RESULT   3
PQ0689
photosystem I 10.4K Hi chain - common tobacco (fragment)
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 17-Mar-1999
C;Accession: PQ0689
R;Obokata, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugiura, M.
Plant Physiol. 102, 1259-1267, 1993
A;Title: Molecular heterogeneity of photosystem I. psaD, psaE, psaF, psaH and psaL are a
A;Reference number: PQ0667; MUID:94105345
A;Accession: PQ0689
A;Molecule type: protein
A;Residues: 1-5 <OBO>
C;Keywords: chloroplast; photosynthesis; photosystem I; thylakoid


  Query Match             44.4%;  Score 12;  DB 2;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 2e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 GD 3
           ||
Db       3 GD 4


RESULT   4
A44692
fulicin - giant African snail
C;Species: Achatina fulica (giant African snail)
C;Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 11-Jul-1997
C;Accession: A44692
R;Ohta, N.; Kubota, I.; Takao, T.; Shimonishi, Y.; Yasuda-Kamatani, Y.; Minakata, H.; No
Biochem. Biophys. Res. Commun. 178, 486-493, 1991
A;Title: Fulicin, a novel neuropeptide containing a D-amino acid residue isolated from t
A;Reference number: A44692; MUID:91315471
A;Accession: A44692
A;Molecule type: protein
A;Residues: 1-5 <OHT>
C;Keywords: amidated carboxyl end; D-amino acid; neuropeptide
F;2/Modified site: D-asparagine (Asn) #status experimental
F;5/Modified site: amidated carboxyl end (Val) #status experimental


  Query Match             44.4%;  Score 12;  DB 2;  Length 5;
  Best Local Similarity   66.7%;  Pred. No. 2e+05;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 DFV 5
           :||
Db       3 EFV 5


RESULT   5
B61445
Leu-enkephalin - blue mussel
C;Species: Mytilus edulis (blue mussel)
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 21-Jan-2000
C;Accession: B61445
R;Leung, M.K.; Stefano, G.B.
Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984
A;Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edul
A;Reference number: A61445; MUID:84144823
A;Accession: B61445
A;Molecule type: protein
A;Residues: 1-5 <LEU>
A;Experimental source: pedal ganglia
C;Keywords: neuropeptide; opioid peptide


  Query Match             44.4%;  Score 12;  DB 2;  Length 5;
  Best Local Similarity   50.0%;  Pred. No. 2e+05;
  Matches    2;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 GDFV 5
           | |:
Db       2 GGFL 5


RESULT   6
A61445
Met-enkephalin - blue mussel
C;Species: Mytilus edulis (blue mussel)
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 21-Jan-2000
C;Accession: A61445
R;Leung, M.K.; Stefano, G.B.
Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984
A;Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edul
A;Reference number: A61445; MUID:84144823
A;Accession: A61445
A;Molecule type: protein
A;Residues: 1-5 <LEU>
A;Experimental source: pedal ganglia
C;Keywords: neuropeptide; opioid peptide


  Query Match             44.4%;  Score 12;  DB 2;  Length 5;
  Best Local Similarity   50.0%;  Pred. No. 2e+05;
  Matches    2;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 GDFV 5
           | |:
Db       2 GGFM 5


RESULT   7
PT0513
T-cell receptor beta chain V-D-J region (100-4AL) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0513; PT0606
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A;Reference number: PT0509; MUID:91277601
A;Accession: PT0513
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <FEE>
A;Experimental source: adult thymus, strain BALB/c, clone 100-4AL
A;Accession: PT0606
A;Status: translation not shown
A;Molecule type: mRNA
```

A;Residues: 1-5 <FE2>
A;Experimental source: newborn thymus, strain BALB/c, clone 120-1S
C;Keywords: T-cell receptor

Query Match 44.4%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GD 3
||
Db 3 GD 4

RESULT 8
PT0538
T-cell receptor beta chain V-D-J region (126-1F) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0538; PT0539; PT0603
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601
A;Accession: PT0538
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <FEE>
A;Experimental source: day 13 fetal thymus, strain BALB/c, clone 126-1F
A;Accession: PT0539
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <FE3>
A;Experimental source: day 18 fetal thymus, strain BALB/c, clone 126-1H
A;Accession: PT0603
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <FE2>
A;Experimental source: newborn thymus, strain BALB/c, clone 100-2AC
C;Keywords: T-cell receptor

Query Match 44.4%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GD 3
||
Db 3 GD 4

RESULT 9
PT0703
T-cell receptor beta chain V-D-J region (135-1F) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0703
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601
A;Accession: PT0703
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-5 <FEE>
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 44.4%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GD 3
||
Db 3 GD 4

RESULT 10
PT0690
T-cell receptor beta chain V-D-J region (140-1BD) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0690
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A;Reference number: PT0509; MUID:91277601
A;Accession: PT0690
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-5 <FEE>
A;Experimental source: day 18 fetal thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 44.4%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GD 3
||
Db 3 GD 4

RESULT 11
PT0573
T-cell receptor beta chain V-D-J region (141-1CC) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0573
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A;Reference number: PT0509; MUID:91277601
A;Accession: PT0573
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <FEE>
A;Experimental source: day 19 fetal thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 44.4%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GD 3
||
Db 3 GD 4

RESULT 12
PT0679
T-cell receptor beta chain V-D-J region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0679; PT0708
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A;Reference number: PT0509; MUID:91277601
A;Accession: PT0679
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-5 <FEE>

A;Experimental source: day 18 fetal thymus, strain BALB/c, 154-2J
A;Accession: PT0708
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-5 <FE2>
A;Experimental source: newborn thymus, strain BALB/c, 161-2B
C;Keywords: T-cell receptor

Query Match 44.4%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GD 3
||
Db 3 GD 4

RESULT 13
ECXAA
antho-RFamide neuropeptide - sea anemone (Anthopleura elegantissima)
C;Species: Anthopleura elegantissima
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 08-Dec-1995
C;Accession: A26666
R;Grimmelikhuijzen, C.J.P.; Graff, D.
Proc. Natl. Acad. Sci. U.S.A. 83, 9817-9821, 1986
A;Title: Isolation of <Glu-Gly-Arg-Phe-NH2 (Antho-RFamide), a neuropeptide from sea anem
A;Reference number: A26666; MUID:87092339
A;Accession: A26666
A;Molecule type: protein
A;Residues: 1-4 <GRI>
C;Comment: The function of this peptide is not known but it could act as a transmitter a
C;Comment: Synthetic and natural peptides had identical properties.
C;Superfamily: RFamide neuropeptide
C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;4/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 40.7%; Score 11; DB 1; Length 4;
Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RGDF 4
:| |
Db 1 QGRF 4

RESULT 14
A25844
autho-RF amide neuropeptide - sea pansy (Renilla koellikeri)
C;Species: Renilla koellikeri (Koelliker's sea pansy)
C;Date: 21-May-1988 #sequence_revision 30-Sep-1993 #text_change 11-Jul-1997
C;Accession: A25844
R;Grimmelikhuijzen, C.J.P.; Groeger, A.
FEBS Lett. 211, 105-108, 1987
A;Title: Isolation of the neuropeptide pGlu-Gly-Arg-Phe-amide from the pennatulid Renill
A;Reference number: A25844
A;Accession: A25844
A;Molecule type: protein
A;Residues: 1-4 <GRI>
C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;4/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 40.7%; Score 11; DB 2; Length 4;
Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RGDF 4
:| |
Db 1 QGRF 4

RESULT 15
S39390
myosin-light-chain kinase (EC 2.7.1.117), smooth muscle - turkey (fragment)
C;Species: Meleagris gallopavo (common turkey)
C;Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 07-May-1999
C;Accession: S39390
R;Komatsu, H.; Ikebe, M.
Biochem. J. 296, 53-58, 1993
A;Title: Affinity labelling of smooth-muscle myosin light-chain kinase with 5'-[p-(f
A;Reference number: S39390; MUID:94071841
A;Accession: S39390
A;Molecule type: protein
A;Residues: 1-4 <KOM>
A;Experimental source: gizzard
C;Keywords: phosphotransferase; smooth muscle

Query Match 40.7%; Score 11; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 2e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GDF 4
| |
Db 2 GKF 4

Search completed: March 6, 2001, 09:47:29
Job time: 155 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: March 6, 2001, 09:45:22 ; Search time 12.72 Seconds
(without alignments)
12.694 Million cell updates/sec

Title: US-09-081-522-5
Perfect score: 27
Sequence: 1 RGDFV 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 28

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	12	44.4	5	1	UXA4_CHLTR	P38005 chlamydia t
2	10	37.0	5	1	TPIS_CANFA	P54714 canis famil
3	9	33.3	5	1	PAP2_PARMA	P81864 pardachirus
4	8	29.6	5	1	TRM3_ECOLI	P13973 escherichia
5	7	25.9	4	1	FLRF_HIRME	P42561 hirudo medi
6	7	25.9	4	1	FMRF_MACNI	P01162 macrocallis
7	6	22.2	3	1	GRWM_HUMAN	P01157 homo sapien
8	6	22.2	3	1	LUXE_VIBFI	P24272 vibrio fisc
9	6	22.2	4	1	ACH1_ACHFU	P35904 achatina fu
10	6	22.2	4	1	DCML_PSECH	P19916 pseudomonas
11	6	22.2	4	1	EOSI_HUMAN	P02731 homo sapien
12	6	22.2	4	1	FAR3_HIRME	P42562 hirudo medi
13	6	22.2	4	1	FAR4_HIRME	P42563 hirudo medi
14	6	22.2	5	1	AL14_CARMA	P81817 carcinus ma
15	6	22.2	5	1	BIOA_CITFR	P13071 citrobacter
16	6	22.2	5	1	BIOA_SALTY	P12677 salmonella
17	6	22.2	5	1	FARP_ARTTR	P41853 artioposthi
18	6	22.2	5	1	SUGA_ACHDO	P19991 acheta dome
19	6	22.2	5	1	UC22_MAIZE	P80628 zea mays (m
20	6	22.2	5	1	UF01_MOUSE	P38639 mus musculu
21	5	18.5	4	1	TUFT_HUMAN	P01858 homo sapien
22	5	18.5	5	1	BIOB_SALTY	P12678 salmonella
23	5	18.5	5	1	PRCT_PERAM	P01373 periplaneta
24	4	14.8	4	1	RM01_YEAST	P36515 saccharomyc
25	2	7.4	4	1	DCMS_PSECH	P19918 pseudomonas
26	2	7.4	5	1	BPP7_BOTIN	P30425 bothrops in
27	1	3.7	3	1	THYL_PIG	P01151 sus scrofa
28	1	3.7	5	1	BIOB_CITFR	P12997 citrobacter

ALIGNMENTS

```
RESULT   1
UXA4_CHLTR
ID   UXA4_CHLTR     STANDARD;      PRT;     5 AA.
AC   P38005;
DT   01-OCT-1994 (Rel. 30, Created)
DT   01-OCT-1994 (Rel. 30, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   UNKNOWN PROTEIN FROM 2D-PAGE FROM ELEMENTARY BODY (FRAGMENT).
OS   Chlamydia trachomatis.
OC   Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
RN   [1]
RP   SEQUENCE.
RC   STRAIN=L2/434/BU;
RA   Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,
RA   Comanducci M., Christianen G., Birkelund S., Vtretou E., Ratti G.,
RA   Pallini V.;
RL   Submitted (SEP-1994) to the SWISS-PROT data bank.
CC   -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC       PROTEIN IS: 4.5, ITS MW IS: 28 KDA.
FT   NON_TER       5       5
SQ   SEQUENCE   5 AA;  474 MW;  75BAA865AA800000 CRC64;


  Query Match             44.4%;  Score 12;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 8.9e+04;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 GD 3
           ||
Db       3 GD 4


RESULT   2
TPIS_CANFA
ID   TPIS_CANFA     STANDARD;      PRT;     5 AA.
AC   P54714;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   TRIOSEPHOSPHATE ISOMERASE (EC 5.3.1.1) (TIM) (FRAGMENT).
GN   TPI1.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
RN   [1]
RP   SEQUENCE.
RC   TISSUE=HEART;
RX   MEDLINE=98163340; PubMed=9504812;
RA   Dunn M.J., Corbett J.M., Wheeler C.H.;
RT   "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT   dog heart proteins.";
RL   Electrophoresis 18:2795-2802(1997).
CC   -!- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE = DIHYDROXY-
CC       ACETONE PHOSPHATE.
CC   -!- PATHWAY: PLAYS AN IMPORTANT ROLE IN SEVERAL METABOLIC PATHWAYS.
CC   -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.
DR   HSC-2DPAGE; P54714; DOG.
DR   INTERPRO; IPR000652; -.
DR   PROSITE; PS00171; TIM; PARTIAL.
KW   Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
KW   Pentose shunt.
FT   NON_TER       1       1
FT   NON_TER       5       5
SQ   SEQUENCE   5 AA;  550 MW;  54444862C9A00000 CRC64;


  Query Match             37.0%;  Score 10;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 8.9e+04;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 FV 5
           ||
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```
Db      1 FV 2


RESULT   3
PAP2_PARMA
ID   PAP2_PARMA     STANDARD;      PRT;     5 AA.
AC   P81864;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   01-OCT-2000 (Rel. 40, Last annotation update)
DE   PARDAXIN II (PXII) (FRAGMENT).
OS   Pardachirus marmoratus (Red sea moses sole).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC   Soleoidei; Soleidae; Pardachirus.
RN   [1]
RP   SEQUENCE.
RC   TISSUE=SKIN SECRETION;
RX   MEDLINE=87057369; PubMed=3782138;
RA   Lazarovici P., Primor N., Loew L.M.;
RT   "Purification and pore-forming activity of two hydrophobic
RT   polypeptides from the secretion of the Red sea moses sole (Pardachirus
RT   marmoratus).";
RL   J. Biol. Chem. 261:16704-16713(1986).
CC   -!- FUNCTION: EXHIBITS UNUSUAL SHARK REPELLENT AND SURFACTANT
CC       PROPERTIES. FORMS VOLTAGE-DEPENDENT, ION-PERMEABLE CHANNELS
CC       IN MEMBRANES. AT HIGH CONCENTRATION CAUSES CELL MEMBRANE LYSIS.
CC   -!- SUBUNIT: MONOMER. IN AQUEOUS SOLUTION EXISTS AS A TETRAMER.
CC   -!- SUBCELLULAR LOCATION: SECRETED.
CC   -!- SIMILARITY: BELONGS TO THE PARDAXIN FAMILY.
KW   Toxin.
FT   NON_TER       5       5
SQ   SEQUENCE   5 AA;  614 MW;  7769C9C9C8100000 CRC64;


  Query Match             33.3%;  Score 9;  DB 1;  Length 5;
  Best Local Similarity   66.7%;  Pred. No. 8.9e+04;
  Matches    2;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 GDF 4
          | |
Db      1 GFF 3


RESULT   4
TRM3_ECOLI
ID   TRM3_ECOLI     STANDARD;      PRT;     5 AA.
AC   P13973;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   TRAM PROTEIN (FRAGMENT).
GN   TRAM.
OS   Escherichia coli.
OG   Plasmid IncFII R100.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Escherichia.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88227859; PubMed=2836369;
RA   Inamoto S., Yoshioka Y., Ohtsubo E.;
RT   "Identification and characterization of the products from the traJ
RT   and traY genes of plasmid R100.";
RL   J. Bacteriol. 170:2749-2757(1988).
CC   -!- FUNCTION: TRANSFER GENE PROTEIN. IS INVOLVED IN THE CONJUGATION
CC       PROCESS OF BACTERIAL CELLS FOR THE EXCHANGE OF PLASMID DNA.
CC   -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC   -!- SIMILARITY: TO TRAM PROTEIN OF OTHER PLASMIDS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M20941; -; NOT_ANNOTATED_CDS.
DR   PIR; A32014; A32014.
KW   Conjugation; Plasmid; DNA-binding.
FT   NON_TER       1       1
SQ   SEQUENCE   5 AA;  634 MW;  6B1B1AA443500000 CRC64;


  Query Match             29.6%;  Score 8;  DB 1;  Length 5;
  Best Local Similarity   33.3%;  Pred. No. 8.9e+04;
  Matches    1;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 RGD 3
            : |
Db      1 KND 3


RESULT   5
FLRF_HIRME
ID   FLRF_HIRME     STANDARD;      PRT;     4 AA.
AC   P42561;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   01-NOV-1995 (Rel. 32, Last annotation update)
DE   FLRFAMIDE.
OS   Hirudo medicinalis (Medicinal leech), and Helisoma trivolvis (Snail).
OC   Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC   Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
RN   [1]
RP   SEQUENCE.
RC   SPECIES=H.MEDICINALIS;
RX   MEDLINE=92195954; PubMed=1686933;
RA   Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT   "Identification of RFamide neuropeptides in the medicinal leech.";
RL   Peptides 12:897-908(1991).
RN   [2]
RP   SEQUENCE.
RC   SPECIES=H.TRIVOLVIS; TISSUE=KIDNEY;
RX   MEDLINE=94286417; PubMed=7912428;
RA   Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT   "FMRFamide-related peptides from the kidney of the snail, Helisoma
RT   trivolvis.";
RL   Peptides 15:31-36(1994).
CC   -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC       FAMILY.
KW   Neuropeptide; Amidation.
FT   MOD_RES       4       4       AMIDATION.
SQ   SEQUENCE   4 AA;  582 MW;  69D40729A0000000 CRC64;


  Query Match             25.9%;  Score 7;  DB 1;  Length 4;
  Best Local Similarity   50.0%;  Pred. No. 8.9e+04;
  Matches    1;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 FV 5
            |:
Db      1 FL 2


RESULT   6
FMRF_MACNI
ID   FMRF_MACNI     STANDARD;      PRT;     4 AA.
AC   P01162;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   FMRFAMIDE (PEAK C) (CARDIOEXCITATORY NEUROPEPTIDE).
OS   Macrocallista nimbosa (Sun-ray clam), Nereis virens (Sandworm),
OS   Hirudo medicinalis (Medicinal leech), and Helisoma trivolvis (Snail).
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OC   Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroida;
OC   Veneroidea; Veneridae; Macrocallista.
RN   [1]
RP   SEQUENCE, AND SYNTHESIS.
RC   SPECIES=M.NIMBOSA; TISSUE=CEREBRAL PEDAL, AND VISCERAL GANGLION;
RX   MEDLINE=77215956; PubMed=877582;
RA   Price D.A., Greenberg M.J.;
RT   "Structure of a molluscan cardioexcitatory neuropeptide.";
RL   Science 197:670-671(1977).
RN   [2]
RP   SEQUENCE, AND CHARACTERIZATION.
RC   SPECIES=M.NIMBOSA; TISSUE=GANGLION;
RX   MEDLINE=78012038; PubMed=909875;
RA   Price D.A., Greenberg M.J.;
RT   "Purification and characterization of a cardioexcitatory neuropeptide
RT   from the central ganglia of a bivalve mollusc.";
RL   Prep. Biochem. 7:261-281(1977).
RN   [3]
RP   SEQUENCE.
RC   SPECIES=N.VIRENS;
RX   MEDLINE=90259866; PubMed=2342992;
RA   Krajniak K.G., Price D.A.;
RT   "Authentic FMRFamide is present in the polychaete Nereis virens.";
RL   Peptides 11:75-77(1990).
RN   [4]
RP   SEQUENCE.
RC   SPECIES=H.MEDICINALIS;
RX   MEDLINE=92195954; PubMed=1686933;
RA   Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT   "Identification of RFamide neuropeptides in the medicinal leech.";
RL   Peptides 12:897-908(1991).
RN   [5]
RP   SEQUENCE.
RC   SPECIES=H.TRIVOLVIS; TISSUE=KIDNEY;
RX   MEDLINE=94286417; PubMed=7912428;
RA   Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT   "FMRFamide-related peptides from the kidney of the snail, Helisoma
RT   trivolvis.";
RL   Peptides 15:31-36(1994).
CC   -!- FUNCTION: MYOACTIVE; CARDIOEXCITATORY SUBSTANCE. PHARMACOLOGICAL
CC       ACTIVITIES INCLUDE AUGMENTATION, INDUCTION, AND REGULARIZATION OF
CC       CARDIAC CONTRACTION.
CC   -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC       FAMILY.
DR   PIR; A01426; ECNK.
DR   PIR; A60418; A60418.
KW   Neuropeptide; Amidation.
FT   MOD_RES       4       4       AMIDATION.
SQ   SEQUENCE   4 AA;  600 MW;  69D40699A0000000 CRC64;


  Query Match             25.9%;  Score 7;  DB 1;  Length 4;
  Best Local Similarity   50.0%;  Pred. No. 8.9e+04;
  Matches    1;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 FV 5
          |:
Db      1 FM 2


RESULT   7
GRWM_HUMAN
ID   GRWM_HUMAN     STANDARD;      PRT;     3 AA.
AC   P01157;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   21-JUL-1986 (Rel. 01, Last annotation update)
DE   GROWTH-MODULATING PEPTIDE.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=77162369; PubMed=858356;
RA   Schlesinger D.H., Pickart L., Thaler M.M.;
RT   "Growth-modulating serum tripeptide is glycyl-histidyl-lysine.";
RL   Experientia 33:324-325(1977).
CC   -!- MISCELLANEOUS: THIS SERUM TRIPEPTIDE HAS BEEN FOUND TO STIMULATE
CC       GROWTH OF SOME CELL TYPES AND TO INHIBIT OTHER TYPES IN VITRO.
DR   PIR; A01421; GKHU.
SQ   SEQUENCE   3 AA;  340 MW;  6331E81000000000 CRC64;


  Query Match             22.2%;  Score 6;  DB 1;  Length 3;
  Best Local Similarity   100.0%;  Pred. No. 8.9e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 G 2
          |
Db      1 G 1


RESULT   8
LUXE_VIBFI
ID   LUXE_VIBFI     STANDARD;      PRT;     3 AA.
AC   P24272;
DT   01-MAR-1992 (Rel. 21, Created)
DT   01-MAR-1992 (Rel. 21, Last sequence update)
DT   01-OCT-1996 (Rel. 34, Last annotation update)
DE   LONG-CHAIN-FATTY-ACID--LUCIFERIN-COMPONENT LIGASE (EC 6.2.1.19)
DE   (ACYL-PROTEIN SYNTHETASE) (FRAGMENT).
GN   LUXE.
OS   Vibrio fischeri.
OC   Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91072226; PubMed=2254256;
RA   Swartzman E., Kapoor S., Graham A.F., Meighen E.A.;
RT   "A new Vibrio fischeri lux gene precedes a bidirectional termination
RT   site for the lux operon.";
RL   J. Bacteriol. 172:6797-6802(1990).
CC   -!- FUNCTION: ACYL-PROTEIN SYNTHETASE ACTIVATES TETRADECANOIC ACID.
CC       IT IS A COMPONENT OF THE FATTY ACID REDUCTASE COMPLEX RESPONSIBLE
CC       FOR CONVERTING TETRADECANOIC ACID TO THE ALDEHYDE WHICH SERVES AS
CC       SUBSTRATE IN THE LUCIFERASE-CATALYZED REACTION.
CC   -!- CATALYTIC ACTIVITY: ATP + AN ACID + PROTEIN = AMP + PYROPHOSPHATE
CC       + AN ACYL-PROTEIN THIOLESTER.
CC   -!- PATHWAY: SECOND STEP IN THE BIOLUMINESCENT FATTY ACID REDUCTASE
CC       COMPLEX.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; M62812; -; NOT_ANNOTATED_CDS.
KW   Luminescence; Ligase.
FT   NON_TER       1       1
SQ   SEQUENCE   3 AA;  374 MW;  6AA3303000000000 CRC64;


  Query Match             22.2%;  Score 6;  DB 1;  Length 3;
  Best Local Similarity   100.0%;  Pred. No. 8.9e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 D 3
          |
Db      3 D 3


RESULT   9
ACH1_ACHFU
ID   ACH1_ACHFU     STANDARD;      PRT;     4 AA.
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AC   P35904;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   ACHATIN-I.
OS   Achatina fulica (Giant African snail).
OC   Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC   Achatinacea; Achatinidae; Achatina.
RN   [1]
RP   SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.
RC   STRAIN=FERUSSAC; TISSUE=GANGLION;
RX   MEDLINE=89273551; PubMed=2597281;
RA   Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,
RA   Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Li P.,
RA   Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.;
RT   "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina
RT   fulica Ferussac containing a D-amino acid residue.";
RL   Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
RN   [2]
RP   CHARACTERIZATION.
RC   STRAIN=FERUSSAC; TISSUE=HEART ATRIUM;
RX   MEDLINE=91264856; PubMed=1675568;
RA   Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,
RA   Yoshida M., Harada A., Muneoka Y., Kobayashi M.;
RT   "Purification of achatin-I from the atria of the African giant snail,
RT   Achatina fulica, and its possible function.";
RL   Biochem. Biophys. Res. Commun. 177:847-853(1991).
RN   [3]
RP   X-RAY CRYSTALLOGRAPHY.
RX   MEDLINE=93014529; PubMed=1399265;
RA   Ishida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,
RA   Iwashita T., Nomoto K.;
RT   "Crystal structure and molecular conformation of achatin-I
RT   (H-Gly-D-Phe-Ala-Asp-OH), an endogenous neuropeptide containing a
RT   D-amino acid residue.";
RL   Int. J. Pept. Protein Res. 39:258-264(1992).
CC   -!- FUNCTION: NEUROEXCITATORY PEPTIDE; INCREASES THE IMPULSE FREQUENCY
CC       AND PRODUCES A SPIKE BROADENING OF THE IDENTIFIED HEART EXCITATORY
CC       NEURON (PON); ALSO ENHANCES THE AMPLITUDE AND FREQUENCY OF THE
CC       HEART BEAT. HAS ALSO AN EFFECT ON SEVERAL OTHER MUSCLES.
DR   PIR; A32480; A32480.
KW   Hormone; D-amino acid.
FT   MOD_RES       2       2       D-PHENYLALANINE.
SQ   SEQUENCE   4 AA;  408 MW;  6AADD9C810000000 CRC64;


  Query Match             22.2%;  Score 6;  DB 1;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 8.9e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 G 2
          |
Db      1 G 1


RESULT  10
DCML_PSECH
ID   DCML_PSECH     STANDARD;      PRT;     4 AA.
AC   P19916;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   01-DEC-1992 (Rel. 24, Last annotation update)
DE   CARBON MONOXIDE DEHYDROGENASE LARGE CHAIN (EC 1.2.99.2) (FRAGMENT).
OS   Pseudomonas carboxydohydrogena.
OC   Bacteria; Proteobacteria.
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=90055678; PubMed=2818128;
RA   Kraut M., Hugendieck I., Herwig S., Meyer O.;
RT   "Homology and distribution of CO dehydrogenase structural genes in
RT   carboxydotrophic bacteria.";
RL   Arch. Microbiol. 152:335-341(1989).
CC   -!- CATALYTIC ACTIVITY: CO + H(2)O + ACCEPTOR = CO(2) + REDUCED
CC       ACCEPTOR.
CC   -!- COFACTOR: MOLYBDENUM.
CC   -!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
CC       SMALL.
DR   PIR; PL0140; PL0140.
KW   Oxidoreductase; Molybdenum.
FT   NON_TER       4       4
SQ   SEQUENCE   4 AA;  441 MW;  7761E876F0000000 CRC64;


  Query Match             22.2%;  Score 6;  DB 1;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 8.9e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 G 2
          |
Db      2 G 2


RESULT  11
EOSI_HUMAN
ID   EOSI_HUMAN     STANDARD;      PRT;     4 AA.
AC   P02731;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   21-JUL-1986 (Rel. 01, Last annotation update)
DE   EOSINOPHILOTACTIC PEPTIDES.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=76078412; PubMed=1060093;
RA   Goetzl E.J., Austen K.F.;
RT   "Purification and synthesis of eosinophilotactic tetrapeptides of
RT   human lung tissue: identification as eosinophil chemotactic factor of
RT   anaphylaxis.";
RL   Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).
CC   -!- MISCELLANEOUS: THESE PEPTIDES ARE RELEASED FROM MAST CELLS IN LUNG
CC       (AND OTHER TISSUES) DURING HYPERSENSITIVITY REACTIONS
CC       (ANAPHYLAXIS). THEIR ACTIVITIES, PREFERENTIALLY AFFECTING
CC       EOSINOPHILS, INCLUDE CHEMOTAXIS, CHEMOTACTIC DEACTIVATION, RELEASE
CC       OF ENZYMES, AND STIMULATION OF THE HEXOSE MONOPHOSPHATE SHUNT.
DR   PIR; A03190; ETBUL.
FT   VARIANT       1       1       V -> A (IN OTHER PEPTIDE).
FT                                 /FTId=VAR_005201.
SQ   SEQUENCE   4 AA;  390 MW;  6B05B862A0000000 CRC64;


  Query Match             22.2%;  Score 6;  DB 1;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 8.9e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 G 2
          |
Db      2 G 2


RESULT  12
FAR3_HIRME
ID   FAR3_HIRME     STANDARD;      PRT;     4 AA.
AC   P42562;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   01-NOV-1995 (Rel. 32, Last annotation update)
DE   FMRFAMIDE-LIKE NEUROPEPTIDE YLRF-AMIDE.
OS   Hirudo medicinalis (Medicinal leech).
OC   Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC   Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=92195954; PubMed=1686933;
RA   Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
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```
RT   "Identification of RFamide neuropeptides in the medicinal leech.";
RL   Peptides 12:897-908(1991).
CC   -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC       FAMILY.
KW   Neuropeptide; Amidation.
FT   MOD_RES       4       4       AMIDATION.
SQ   SEQUENCE   4 AA;  598 MW;  69D4073B30000000 CRC64;


  Query Match             22.2%;  Score 6;  DB 1;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 8.9e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 F 4
          |
Db      4 F 4


RESULT  13
FAR4_HIRME
ID   FAR4_HIRME     STANDARD;      PRT;     4 AA.
AC   P42563;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   01-NOV-1995 (Rel. 32, Last annotation update)
DE   FMRFAMIDE-LIKE NEUROPEPTIDE YMRF-AMIDE.
OS   Hirudo medicinalis (Medicinal leech).
OC   Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC   Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=92195954; PubMed=1686933;
RA   Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT   "Identification of RFamide neuropeptides in the medicinal leech.";
RL   Peptides 12:897-908(1991).
CC   -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC       FAMILY.
KW   Neuropeptide; Amidation.
FT   MOD_RES       4       4       AMIDATION.
SQ   SEQUENCE   4 AA;  616 MW;  69D4068B30000000 CRC64;


  Query Match             22.2%;  Score 6;  DB 1;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 8.9e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 F 4
          |
Db      4 F 4


RESULT  14
AL14_CARMA
ID   AL14_CARMA     STANDARD;      PRT;     5 AA.
AC   P81817;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   CARCINUSTATIN 14.
OS   Carcinus maenas (Common shore crab) (Green crab).
OC   Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC   Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC   Eubrachyura; Portunoidea; Portunidae; Carcinus.
RN   [1]
RP   SEQUENCE.
RC   TISSUE=CEREBRAL GANGLION, AND THORACIC GANGLION;
RX   MEDLINE=98121193; PubMed=9461295;
RA   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA   Thorpe A.;
RT   "Isolation and identification of multiple neuropeptides of the
RT   allatostatin superfamily in the shore crab Carcinus maenas.";
RL   Eur. J. Biochem. 250:727-734(1997).
CC   -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC   -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW   Neuropeptide; Amidation; Multigene family.
FT   MOD_RES       5       5       AMIDATION (POTENTIAL).
SQ   SEQUENCE   5 AA;  586 MW;  672879D5AB300000 CRC64;


  Query Match             22.2%;  Score 6;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 8.9e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 F 4
          |
Db      3 F 3


RESULT  15
BIOA_CITFR
ID   BIOA_CITFR     STANDARD;      PRT;     5 AA.
AC   P13071;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   01-DEC-1992 (Rel. 24, Last annotation update)
DE   ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE
DE   (EC 2.6.1.62) (7,8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA
DE   AMINOTRANSFERASE) (FRAGMENT).
GN   BIOA.
OS   Citrobacter freundii.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Citrobacter.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89005280; PubMed=2971595;
RA   Shiuan D., Campbell A.;
RT   "Transcriptional regulation and gene arrangement of Escherichia coli,
RT   Citrobacter freundii and Salmonella typhimurium biotin operons.";
RL   Gene 67:203-211(1988).
CC   -!- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + 8-AMINO-7-
CC       OXONONANOATE = S-ADENOSYL-4-METHYLTHIO-2-OXOBUTANOATE +
CC       7,8-DIAMINONONANOATE.
CC   -!- COFACTOR: PYRIDOXAL PHOSPHATE.
CC   -!- PATHWAY: BIOTIN BIOSYNTHESIS.
CC   -!- SUBUNIT: HOMODIMER.
CC   -!- SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC       AMINOTRANSFERASES.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; M21922; CAB25179.1; -.
DR   INTERPRO; IPR000954; -.
DR   PROSITE; PS00600; AA_TRANSFER_CLASS_3; PARTIAL.
KW   Biotin biosynthesis; Transferase; Aminotransferase;
KW   Pyridoxal phosphate.
FT   NON_TER       5       5
SQ   SEQUENCE   5 AA;  582 MW;  5AAAB1B1A6F00000 CRC64;


  Query Match             22.2%;  Score 6;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 8.9e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 D 3
          |
Db      4 D 4


Search completed: March 6, 2001, 09:48:22
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Job time: 180 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: March 6, 2001, 09:44:54 ; Search time 32.72 Seconds
(without alignments)
17.911 Million cell updates/sec

Title: US-09-081-522-5
Perfect score: 27
Sequence: 1 RGDFV 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 8

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_15:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	12	44.4	5	13	P82070	P82070 litoria rub
2	10	37.0	5	13	P82099	P82099 litoria rub
3	9	33.3	5	13	P82073	P82073 litoria rub
4	9	33.3	5	13	P82100	P82100 litoria rub
5	8	29.6	5	13	P82071	P82071 litoria rub
6	8	29.6	5	13	P82072	P82072 litoria rub
7	4	14.8	4	11	Q08433	Q08433 rattus norv
8	2	7.4	5	10	Q99007	Q99007 hordeum vul

ALIGNMENTS

RESULT 1
P82070
ID P82070 PRELIMINARY; PRT; 5 AA.
AC P82070;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE RUBELLIDIN 1.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=SKIN SECRETION;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australin red tree frog
RT 'Litoria rubella'. the skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
CC -!- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
CC ANTIBIOTIC ACTIVITY.
CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -!- MASS SPECTROMETRY: MW=598; METHOD=FAB.
KW Amphibian skin.
SQ SEQUENCE 5 AA; 598 MW; 6DD9C9CAB2A00000 CRC64;

Query Match 44.4%; Score 12; DB 13; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DF 4
||
Db 2 DF 3

RESULT 2
P82099
ID P82099 PRELIMINARY; PRT; 5 AA.
AC P82099;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE ELECTRIN 3.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=SKIN SECRETION;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litori electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:0-0(1999).
KW Amphibian skin; Amidation.
FT MOD_RES 5 5 AMIDATION.
SQ SEQUENCE 5 AA; 630 MW; 668761F2C9A00000 CRC64;

Query Match 37.0%; Score 10; DB 13; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FV 5
||
Db 1 FV 2

RESULT 3
P82073
ID P82073 PRELIMINARY; PRT; 5 AA.
AC P82073;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)

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DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   RUBELLIDIN 3.2.
OS   Litoria rubella (Desert tree frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC   Litoria.
OX   NCBI_TaxID=104895;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=SKIN SECRETION;
RA   Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT   "Peptides from the skin glands of the Australian buzzing tree frog
RT   Litori electrica. Comparison with the skin peptides from Litoria
RT   rubella.";
RL   Aust. J. Chem. 52:0-0(1999).
CC   -!- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
CC       ANTIBIOTIC ACTIVITY.
CC   -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
KW   Amphibian skin.
SQ   SEQUENCE   5 AA;  570 MW;  71A9C9C862A00000 CRC64;


  Query Match             33.3%;  Score 9;  DB 13;  Length 5;
  Best Local Similarity   66.7%;  Pred. No. 3.7e+05;
  Matches    2;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 GDF 4
          | |
Db      2 GFF 4


RESULT   4
P82100
ID   P82100      PRELIMINARY;      PRT;     5 AA.
AC   P82100;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   ELECTRIN 4.
OS   Litoria rubella (Desert tree frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC   Litoria.
OX   NCBI_TaxID=104895;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=SKIN SECRETION;
RA   Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT   "Peptides from the skin glands of the Australian buzzing tree frog
RT   Litori electrica. Comparison with the skin peptides from Litoria
RT   rubella.";
RL   Aust. J. Chem. 52:0-0(1999).
KW   Amphibian skin; Amidation.
FT   MOD_RES       5       5       AMIDATION.
SQ   SEQUENCE   5 AA;  616 MW;  61F2D1A059A00000 CRC64;


  Query Match             33.3%;  Score 9;  DB 13;  Length 5;
  Best Local Similarity   50.0%;  Pred. No. 3.7e+05;
  Matches    1;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 FV 5
          |:
Db      1 FI 2


RESULT   5
P82071
ID   P82071      PRELIMINARY;      PRT;     5 AA.
AC   P82071;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   RUBELLIDIN 2.1.
OS   Litoria rubella (Desert tree frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC   Litoria.
OX   NCBI_TaxID=104895;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=SKIN SECRETION;
RA   Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA   Tyler M.J., Wallace J.C.;
RT   "The structure of new peptides from the Australin red tree frog
RT   'Litoria rubella'. the skin peptide profile as a probe for the study
RT   of evolutionary trends of amphibians.";
RL   Aust. J. Chem. 49:955-963(1996).
CC   -!- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
CC       ANTIBIOTIC ACTIVITY.
CC   -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC   -!- MASS SPECTROMETRY: MW=626; METHOD=FAB.
KW   Amphibian skin.
SQ   SEQUENCE   5 AA;  626 MW;  6DD9C9CB10300000 CRC64;


  Query Match             29.6%;  Score 8;  DB 13;  Length 5;
  Best Local Similarity   50.0%;  Pred. No. 3.7e+05;
  Matches    1;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 DF 4
          :|
Db      2 EF 3


RESULT   6
P82072
ID   P82072      PRELIMINARY;      PRT;     5 AA.
AC   P82072;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   RUBELLIDIN 3.1.
OS   Litoria rubella (Desert tree frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC   Litoria.
OX   NCBI_TaxID=104895;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=SKIN SECRETION;
RA   Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA   Tyler M.J., Wallace J.C.;
RT   "The structure of new peptides from the Australin red tree frog
RT   'Litoria rubella'. the skin peptide profile as a probe for the study
RT   of evolutionary trends of amphibians.";
RL   Aust. J. Chem. 49:955-963(1996).
CC   -!- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
CC       ANTIBIOTIC ACTIVITY.
CC   -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC   -!- MASS SPECTROMETRY: MW=655; METHOD=FAB.
KW   Amphibian skin; Amidation.
FT   MOD_RES       5       5       AMIDATION.
SQ   SEQUENCE   5 AA;  656 MW;  71A9C9CB10300000 CRC64;


  Query Match             29.6%;  Score 8;  DB 13;  Length 5;
  Best Local Similarity   50.0%;  Pred. No. 3.7e+05;
  Matches    1;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 DF 4
          :|
Db      2 EF 3
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RESULT   7
Q08433
ID   Q08433      PRELIMINARY;      PRT;     4 AA.
AC   Q08433;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
DE   UDP-GLUCURONOSYLTRANSFERASE, MICROSOMAL (EC 2.4.1.17) (UDPGT)
DE   (FRAGMENT).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=GUNN;
RX   MEDLINE=91282758; PubMed=1840486;
RA   Sato H., Aono S., Kashiwamata S., Koiwai O.;
RT   "Genetic defect of bilirubin UDP-glucuronosyltransferase in the
RT   hyperbilirubinemic Gunn rat.";
RL   Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
CC   -!- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
CC       SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
CC       ENDOGENOUS COMPOUNDS.
CC   -!- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
CC       BETA-D-GLUCORONOSIDE.
CC   -!- SUBCELLULAR LOCATION: MICROSOME.
DR   EMBL; S38636; AAB19259.1; -.
KW   Transferase; Glycosyltransferase; Microsome; Multigene family.
FT   NON_TER       1      1
FT   NON_TER       4      4
SQ   SEQUENCE   4 AA;  473 MW;  633732C420000000 CRC64;


  Query Match             14.8%;  Score 4;  DB 11;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 V 5
          |
Db      2 V 2


RESULT   8
Q99007
ID   Q99007      PRELIMINARY;      PRT;     5 AA.
AC   Q99007;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   ALPHA-AMYLASE (EC 3.2.1.1) (FRAGMENT).
GN   AMY1.
OS   Hordeum vulgare (Barley).
OC   Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC   Magnoliophyta; Liliopsida; Poales; Poaceae; Hordeum.
OX   NCBI_TaxID=4513;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=HIMALAYA; TISSUE=ALEURONE LAYER;
RX   MEDLINE=91329704; PubMed=1831055;
RA   Jacobsen J.V., Close T.J.;
RT   "Control of transient expression of chimaeric genes by gibberellic
RT   acid and abscisic acid in protoplasts prepared from mature barley
RT   aleurone layers.";
RL   Plant Mol. Biol. 16:713-721(1991).
CC   -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC
CC       LINKAGES IN OLIGOSACCHARIDES AND POLYASACCHARIDES.
CC   -!- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC   -!- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN
CC       BARLEY.
DR   EMBL; X54643; CAA38455.1; -.
KW   Hydrolase; Glycosidase; Carbohydrate metabolism; Seed; Germination;
KW   Calcium; Multigene family.
FT   NON_TER       5      5
SQ   SEQUENCE   5 AA;  600 MW;  61E3344DD6F00000 CRC64;


  Query Match             7.4%;  Score 2;  DB 10;  Length 5;
  Best Local Similarity   0.0%;  Pred. No. 3.7e+05;
  Matches    0;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 R 1
          :
Db      4 K 4


Search completed: March  6, 2001, 09:48:05
Job time: 191 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: March 6, 2001, 09:45:52 ; Search time 30.08 Seconds
(without alignments)
5.684 Million cell updates/sec

Title: US-09-081-522-7
Perfect score: 27
Sequence: 1 RGDFV 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 14863

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_36:*
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2: /SIDS1/gcgdata/geneseq/geneseqp/AA1981.DAT:*
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5: /SIDS1/gcgdata/geneseq/geneseqp/AA1984.DAT:*
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7: /SIDS1/gcgdata/geneseq/geneseqp/AA1986.DAT:*
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19: /SIDS1/gcgdata/geneseq/geneseqp/AA1998.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseqp/AA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqp/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	27	100.0	5	15	R45382	Cell adhesion inhi
2	27	100.0	5	15	R45384	Cell adhesion inhi
3	27	100.0	5	15	R45386	Cell adhesion inhi
4	27	100.0	5	15	R45387	Cell adhesion inhi
5	27	100.0	5	16	R82387	Cyclic integrin al
6	27	100.0	5	16	R82389	Cyclic integrin al
7	27	100.0	5	18	W33057	Alpha-v, beta-5 vi
8	27	100.0	5	18	W33055	Alpha-v, beta-5 vi
9	27	100.0	5	19	W41099	Alpha-v beta-3 ant
10	27	100.0	5	19	W41101	Alpha-v beta-3 ant
11	27	100.0	5	19	W41109	Alpha-v beta-3 ant
12	27	100.0	5	19	W41240	Alpha-v-beta-5 ant
13	27	100.0	5	19	W41243	Alpha-v-beta-5 ant
14	27	100.0	5	19	W41247	Alpha-v-beta-5 ant
15	27	100.0	5	20	W92307	Cyclic azapeptide
16	24	88.9	5	20	W92302	Cyclic adhesion in
17	24	88.9	5	20	W92306	Cyclic adhesion in
18	23	85.2	4	12	R10408	Fibrinogen recepto
19	23	85.2	4	13	R25316	Cell contact inhib
20	23	85.2	4	14	R32385	Fibrinogen recepto
21	23	85.2	4	14	R69333	Gp IIb/IIIa recept
22	23	85.2	4	15	R54528	Platelet aggregati
23	23	85.2	4	15	R49800	Sequence of peptid
24	23	85.2	4	15	R42568	Tri-/tetra-cyclic
25	23	85.2	4	18	W25179	RGD-peptide capabl
26	23	85.2	4	19	W52096	Targetting peptide
27	23	85.2	4	19	W50599	GPIIb/IIIa recepto
28	23	85.2	5	12	R10179	RGD-contg. peptide
29	23	85.2	5	12	R11760	Peptide #4 having
30	23	85.2	5	13	R24515	Platelet antagonis
31	23	85.2	5	18	Y08052	Biotin derivative
32	23	85.2	5	18	Y08055	Biotin derivative
33	23	85.2	5	18	W35358	Cyclic integrin an
34	23	85.2	5	18	W35359	Cyclic integrin an
35	23	85.2	5	18	W35355	Cyclic integrin an
36	23	85.2	5	18	W35356	Cyclic integrin an
37	23	85.2	5	18	W35357	Cyclic integrin an
38	23	85.2	5	18	W35353	Cyclic integrin an
39	23	85.2	5	18	W35354	Cyclic integrin an
40	23	85.2	5	18	W35352	Cyclic integrin an
41	23	85.2	5	18	W13156	Integrin inhibitin
42	23	85.2	5	18	W13160	Integrin inhibitin
43	23	85.2	5	19	W41110	Cyclic peptide 112
44	23	85.2	5	19	W41246	Alpha-v-beta-5 ant
45	23	85.2	5	20	Y43231	RGD-containing pep

ALIGNMENTS

RESULT 1
R45382
ID R45382 standard; Protein; 5 AA.
XX
AC R45382;
XX
DT 06-JUL-1994 (first entry)
XX
DE Cell adhesion inhibition peptide (m).
XX
KW Cyclopentapeptide; cyclohexapeptide; inhibition; adhesion;
KW animal; somatic; cell; thrombosis; myocardial infarction;
KW apoplexy; arteriosclerosis; inflammation; angina pectoris;
KW osteoporosis; tumour; adhesion-receptor antagonist; osteoclast;
KW wound healing; beta-3 integrin; fibrogen binding.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "D-form residue, Amide linkage to Val5 forming
FT a cyclic peptide"
FT Modified-site 5
FT /note= "Amide linkage to Arg1 forming a cyclic peptide"
XX
PN EP578083-A.
XX
PD 12-JAN-1994.
XX
PF 26-JUN-1993; 93EP-0110232.
XX
PR 06-JUL-1992; 92US-0909367.
PR 24-FEB-1993; 93US-0022024.
XX
PA (MERE) MERCK PATENT GMBH.

XX
PI Cheresh DA, Diefenbach B, Felding-Habermann B, Gurrath M;
PI Hoelzemann G, Jonczyk A, Kessler H, Melzer G, Mueller G;
XX
DR WPI; 1994-009982/02.
XX
PT Compsn. contg. cyclopenta- or hexa-peptide - inhibits adhesion of
PT animal cells, used in the treatment and prophylaxis of e.g.
PT thrombosis, tumours, osteoporosis or inflammation
XX
PS Claim 1; Page 7; 9pp; English.
XX
CC The sequences given in R45370-87 are cyclopenta- and
CC cyclohexapeptides which act to inhibit adhesion between animal cells.
CC A composition containing these peptides may be used in the
CC treatment and prophylaxis of thrombosis, myocardial infarction,
CC apoplexy, arteriosclerosis, inflammation, angina pectoris,
CC osteoporosis and/or tumour. They are used to induce an adhesion-
CC receptor antagonist effect in the subject, to inhibit cell adhesion,
CC and in the formation of osteoclasts. They may also be used in wound
CC healing compositions and to block beta-3 integrin fibrogen binding.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 27; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGDFV 5
|||||
Db 1 rgdfv 5

RESULT 2
R45384
ID R45384 standard; Protein; 5 AA.
XX
AC R45384;
XX
DT 06-JUL-1994 (first entry)
XX
DE Cell adhesion inhibition peptide (o).
XX
KW Cyclopentapeptide; cyclohexapeptide; inhibition; adhesion;
KW animal; somatic; cell; thrombosis; myocardial infarction;
KW apoplexy; arteriosclerosis; inflammation; angina pectoris;
KW osteoporosis; tumour; adhesion-receptor antagonist; osteoclast;
KW wound healing; beta-3 integrin; fibrogen binding.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "Amide linkage to Val5 forming a cyclic peptide"
FT Misc-difference 4
FT /note= "D-form residue"
FT Modified-site 5
FT /note= "Amide linkage to Arg1 forming a cyclic peptide"
XX
PN EP578083-A.
XX
PD 12-JAN-1994.
XX
PF 26-JUN-1993; 93EP-0110232.
XX
PR 06-JUL-1992; 92US-0909367.
PR 24-FEB-1993; 93US-0022024.
XX
PA (MERE) MERCK PATENT GMBH.
XX
PI Cheresh DA, Diefenbach B, Felding-Habermann B, Gurrath M;
PI Hoelzemann G, Jonczyk A, Kessler H, Melzer G, Mueller G;
XX
DR WPI; 1994-009982/02.
XX
PT Compsn. contg. cyclopenta- or hexa-peptide - inhibits adhesion of
PT animal cells, used in the treatment and prophylaxis of e.g.
PT thrombosis, tumours, osteoporosis or inflammation
XX
PS Claim 1; Page 7; 9pp; English.
XX
CC The sequences given in R45370-87 are cyclopenta- and
CC cyclohexapeptides which act to inhibit adhesion between animal cells.
CC A composition containing these peptides may be used in the
CC treatment and prophylaxis of thrombosis, myocardial infarction,
CC apoplexy, arteriosclerosis, inflammation, angina pectoris,
CC osteoporosis and/or tumour. They are used to induce an adhesion-
CC receptor antagonist effect in the subject, to inhibit cell adhesion,
CC and in the formation of osteoclasts. They may also be used in wound
CC healing compositions and to block beta-3 integrin fibrogen binding.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 27; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGDFV 5
|||||
Db 1 rgdfv 5

RESULT 3
R45386
ID R45386 standard; Protein; 5 AA.
XX
AC R45386;
XX
DT 06-JUL-1994 (first entry)
XX
DE Cell adhesion inhibition peptide (q).
XX
KW Cyclopentapeptide; cyclohexapeptide; inhibition; adhesion;
KW animal; somatic; cell; thrombosis; myocardial infarction;
KW apoplexy; arteriosclerosis; inflammation; angina pectoris;
KW osteoporosis; tumour; adhesion-receptor antagonist; osteoclast;
KW wound healing; beta-3 integrin; fibrogen binding.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "Amide linkage to Val5 forming a cyclic peptide"
FT Modified-site 5
FT /note= "D-form residue, Amide linkage to Arg1 forming
FT a cyclic peptide"
XX
PN EP578083-A.
XX
PD 12-JAN-1994.
XX
PF 26-JUN-1993; 93EP-0110232.
XX
PR 06-JUL-1992; 92US-0909367.
PR 24-FEB-1993; 93US-0022024.
XX
PA (MERE) MERCK PATENT GMBH.
XX
PI Cheresh DA, Diefenbach B, Felding-Habermann B, Gurrath M;
PI Hoelzemann G, Jonczyk A, Kessler H, Melzer G, Mueller G;
XX
DR WPI; 1994-009982/02.
XX
PT Compsn. contg. cyclopenta- or hexa-peptide - inhibits adhesion of

PT animal cells, used in the treatment and prophylaxis of e.g.
PT thrombosis, tumours, osteoporosis or inflammation
XX
PS Claim 1; Page 7; 9pp; English.
XX
CC The sequences given in R45370-87 are cyclopenta- and
CC cyclohexapeptides which act to inhibit adhesion between animal cells.
CC A composition containing these peptides may be used in the
CC treatment and prophylaxis of thrombosis, myocardial infarction,
CC apoplexy, arteriosclerosis, inflammation, angina pectoris,
CC osteoporosis and/or tumour. They are used to induce an adhesion-
CC receptor antagonist effect in the subject, to inhibit cell adhesion,
CC and in the formation of osteoclasts. They may also be used in wound
CC healing compositions and to block beta-3 integrin fibrogen binding.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 27; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGDFV 5
|||||
Db 1 rgdfv 5

RESULT 4
R45387
ID R45387 standard; Protein; 5 AA.
XX
AC R45387;
XX
DT 06-JUL-1994 (first entry)
XX
DE Cell adhesion inhibition peptide (r).
XX
KW Cyclopentapeptide; cyclohexapeptide; inhibition; adhesion;
KW animal; somatic; cell; thrombosis; myocardial infarction;
KW apoplexy; arteriosclerosis; inflammation; angina pectoris;
KW osteoporosis; tumour; adhesion-receptor antagonist; osteoclast;
KW wound healing; beta-3 integrin; fibrogen binding.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "Amide linkage to Val5 forming a cyclic peptide"
FT Misc-difference 3
FT /note= "D-form residue"
FT Modified-site 5
FT /note= "Amide linkage to Arg1 forming a cyclic peptide"
XX
PN EP578083-A.
XX
PD 12-JAN-1994.
XX
PF 26-JUN-1993; 93EP-0110232.
XX
PR 06-JUL-1992; 92US-0909367.
PR 24-FEB-1993; 93US-0022024.
XX
PA (MERE) MERCK PATENT GMBH.
XX
PI Cheresh DA, Diefenbach B, Felding-Habermann B, Gurrath M;
PI Hoelzemann G, Jonczyk A, Kessler H, Melzer G, Mueller G;
XX
DR WPI; 1994-009982/02.
XX
PT Compsn. contg. cyclopenta- or hexa-peptide - inhibits adhesion of
PT animal cells, used in the treatment and prophylaxis of e.g.
PT thrombosis, tumours, osteoporosis or inflammation
XX
PS Claim 1; Page 7; 9pp; English.
XX
CC The sequences given in R45370-87 are cyclopenta- and
CC cyclohexapeptides which act to inhibit adhesion between animal cells.
CC A composition containing these peptides may be used in the
CC treatment and prophylaxis of thrombosis, myocardial infarction,
CC apoplexy, arteriosclerosis, inflammation, angina pectoris,
CC osteoporosis and/or tumour. They are used to induce an adhesion-
CC receptor antagonist effect in the subject, to inhibit cell adhesion,
CC and in the formation of osteoclasts. They may also be used in wound
CC healing compositions and to block beta-3 integrin fibrogen binding.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 27; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGDFV 5
|||||
Db 1 rgdfv 5

RESULT 5
R82387
ID R82387 standard; peptide; 5 AA.
XX
AC R82387;
XX
DT 03-MAY-1996 (first entry)
XX
DE Cyclic integrin alpha-v-beta-3 inhibitor peptide no. 62184.
XX
KW Integrin; alpha-v-beta-3; inhibitor; angiogenesis; antagonist;
KW fibrinogen; inflammation; apoptosis; restenosis; cyclic.
XX
OS Synthetic.
XX
PN WO9525543-A1.
XX
PD 28-SEP-1995.
XX
PF 09-MAR-1995; 95WO-US03035.
XX
PR 30-DEC-1994; 94US-0366665.
PR 18-MAR-1994; 94US-0210715.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Brooks P, Cheresh DA;
XX
DR WPI; 1995-344463/44.
XX
PT Inhibition of angiogenesis in a tissue, e.g. following angioplasty
PT - by admin. of a compsn. comprising an alpha-v-beta3 antagonist,
PT useful for regression of established tumours, treating inflamed
PT tissue, etc.
XX
PS Claim 4; Page 47; 135pp; English.
XX
CC R82386-96 are a group of inhibitor peptides of integrin alpha-v-beta-3.
CC The inhibitor peptides may be administered in a compsn. and are useful
CC for inhibition of inflamed tissue angiogenesis, e.g. that associated
CC with rheumatoid arthritis, retinal angiogenesis associated with
CC diabetic retinopathy, that associated with haemangioma, solid
CC tumours, or solid tumour metastases. The alpha-v-beta-3 atagonists
CC are also useful to induce apoptosis in neovasculature in a tissue.
CC The inhibitor peptides are pref. cyclic and contain an RGD sequence.
XX
SQ Sequence 5 AA;

```
  Query Match           100.0%;  Score 27;  DB 16;  Length 5;
  Best Local Similarity  100.0%;  Pred. No. 2.1e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RGDFV 5
          |||||
Db      1 rgdfv 5


RESULT   6
R82389.
ID   R82389 standard; peptide; 5 AA.
XX
AC   R82389;
XX
DT   03-MAY-1996  (first entry)
XX
DE   Cyclic integrin alpha-v-beta-3 inhibitor peptide no. 62187.
XX
KW   Integrin; alpha-v-beta-3; inhibitor; angiogenesis; antagonist;
KW   fibrinogen; inflammation; apoptosis; restenosis; cyclic.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 4
FT                   /note= "D-Val"
XX
PN   WO9525543-A1.
XX
PD   28-SEP-1995.
XX
PF   09-MAR-1995;   95WO-US03035.
XX
PR   30-DEC-1994;   94US-0366655.
PR   18-MAR-1994;   94US-0210715.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Brooks P,  Cheresh DA;
XX
DR   WPI; 1995-344463/44.
XX
PT   Inhibition of angiogenesis in a tissue, e.g. following angioplasty
PT   - by admin. of a compsn. comprising an alpha-v-beta3 antagonist,
PT   useful for regression of established tumours, treating inflamed
PT   tissue, etc.
XX
PS   Claim 4; Page 47; 135pp; English.
XX
CC   R82386-96 are a group of inhibitor peptides of integrin alpha-v-beta-3.
CC   The inhibitor peptides may be  administered in a compsn. and are useful
CC   for inhibition of inflamed tissue angiogenesis, e.g. that associated
CC   with rheumatoid arthritis, retinal angiogenesis associated with
CC   diabetic retinopathy, that associated with haemangioma, solid
CC   tumours, or solid tumour metastases. The alpha-v-beta-3 atagonists
CC   are also useful to induce apoptosis in neovasculature in a tissue.
CC   The inhibitor peptides are pref. cyclic and contain an RGD sequence.
XX
SQ   Sequence   5 AA;


  Query Match           100.0%;  Score 27;  DB 16;  Length 5;
  Best Local Similarity  100.0%;  Pred. No. 2.1e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RGDFV 5
          |||||
Db      1 rgdfv 5


RESULT   7
W33057
ID   W33057 standard; peptide; 5 AA.
XX
AC   W33057;
XX
DT   26-JAN-1998  (first entry)
XX
DE   Alpha-v, beta-5 vitronectin receptor antagonist.
XX
KW   RGD containing peptide; antagonist; alpha-v, beta-5;
KW   vitronectin receptor; inhibition; angiogenesis; inflammation;
KW   rheumatoid arthritis; eye disease; diabetic retinopathy;
KW   age related macular degeneration; ocular histoplasmosis;
KW   retinopathy; prematurity; neovascular glaucoma;
KW   corneal neovascular disorder; transplantation; herpetic; luetic;
KW   keratitis; pterygium; neovascular pannus; haemangioma;
KW   solid tumour; metastasis; cytokine; low toxicity;
KW   vascular endothelial growth factor;
KW   transforming growth factor alpha; epidermal growth factor; cyclic.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 5
FT                   /note= "D-form residue"
XX
PN   WO9706791-A1.
XX
PD   27-FEB-1997.
XX
PF   13-AUG-1996;   96WO-US13194.
XX
PR   14-AUG-1995;   95US-0514799.
PR   14-AUG-1996;   96ZA-0006886.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Brooks P,  Cheresh DA,  Friedlander M;
XX
DR   WPI; 1997-165019/15.
XX
PT   Inhibiting angiogenesis with an antagonist selective for the
PT   alpha-v,beta-5 integrin receptor - e.g. antibody, RGD peptide or
PT   organic mimetic, for treatment of inflammation, eye disease, tumours
PT   etc.
XX
PS   Claim 5; Page 105; 126pp; English.
XX
CC   The present RGD containing peptide is an antagonist of the alpha-v,
CC   beta-5 vitronectin receptor, which can be used to inhibit
CC   angiogenesis in alpha-v, beta-5 containing tissue, specifically
CC   angiogenesis as a result of inflammation (especially rheumatoid
CC   arthritis), eye disease (especially diabetic retinopathy, age
CC   related macular degeneration, ocular histoplasmosis, retinopathy of
CC   prematurity or neovascular glaucoma), corneal neovascular disorders
CC   (especially transplantation, herpetic or luetic keratitis,
CC   pterygium and neovascular pannus associated with wearing contact
CC   lenses), haemangioma, solid tumours and their metastases or
CC   cytokines (especially vascular endothelial growth factor,
CC   transforming growth factor alpha or epidermal growth factor). The
CC   antagonist has the advantage of being very specific, affecting no
CC   processes other than angiogenesis and therefore of relatively low
CC   toxicity.
XX
SQ   Sequence   5 AA;


  Query Match           100.0%;  Score 27;  DB 18;  Length 5;
  Best Local Similarity  100.0%;  Pred. No. 2.1e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RGDFV 5
          |||||
Db      1 rgdfv 5
```

```
RESULT   8
W33055
ID   W33055 standard; peptide; 5 AA.
XX
AC   W33055;
XX
DT   26-JAN-1998  (first entry)
XX
DE   Alpha-v, beta-5 vitronectin receptor antagonist.
XX
KW   RGD containing peptide; antagonist; alpha-v, beta-5;
KW   vitronectin receptor; inhibition; angiogenesis; inflammation;
KW   rheumatoid arthritis; eye disease; diabetic retinopathy;
KW   age related macular degeneration; ocular histoplasmosis;
KW   retinopathy; prematurity; neovascular glaucoma;
KW   corneal neovascular disorder; transplantation; herpetic; luetic;
KW   keratitis; pterygium; neovascular pannus; haemangioma;
KW   solid tumour; metastasis; cytokine; low toxicity;
KW   vascular endothelial growth factor;
KW   transforming growth factor alpha; epidermal growth factor; cyclic.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 4
FT                   /note= "D-form residue"
XX
PN   WO9706791-A1.
XX
PD   27-FEB-1997.
XX
PF   13-AUG-1996;   96WO-US13194.
XX
PR   14-AUG-1995;   95US-0514799.
PR   14-AUG-1996;   96ZA-0006886.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Brooks P,  Cheresh DA,  Friedlander M;
XX
DR   WPI; 1997-165019/15.
XX
PT   Inhibiting angiogenesis with an antagonist selective for the
PT   alpha-v,beta-5 integrin receptor - e.g. antibody, RGD peptide or
PT   organic mimetic, for treatment of inflammation, eye disease, tumours
PT   etc.
XX
PS   Claim 5; Page 105; 126pp; English.
XX
CC   The present RGD containing peptide is an antagonist of the alpha-v,
CC   beta-5 vitronectin receptor, which can be used to inhibit
CC   angiogenesis in alpha-v, beta-5 containing tissue, speicfically
CC   angiogenesis as a result of inflammation (especially rheumatoid
CC   arthritis), eye disease (especially diabetic retinopathy, age
CC   related macular degeneration, ocular histoplasmosis, retinopathy of
CC   prematurity or neovascular glaucoma), corneal neovascular disorders
CC   (especially transplantation, herpetic or luetic keratitis,
CC   pterygium and neovascular pannus associated with wearing contact
CC   lenses), haemangioma, solid tumours and their metastases or
CC   cytokines (especially vascular endothelial growth factor,
CC   transforming growth factor alpha or epidermal growth factor). The
CC   antagonist has the advantage of being very specific, affecting no
CC   processes other than angiogenesis and therefore of relatively low
CC   toxicity.
XX
SQ   Sequence   5 AA;

  Query Match           100.0%;  Score 27;  DB 18;  Length 5;
  Best Local Similarity  100.0%;  Pred. No. 2.1e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RGDFV 5
           |||||
Db       1 rgdfv 5


RESULT   9
W41099
ID   W41099 standard; Peptide; 5 AA.
XX
AC   W41099;
XX
DT   08-JUN-1998  (first entry)
XX
DE   Alpha-v beta-3 antagonist cyclic peptide 62184 (66203).
XX
KW   Angiogenesis; inhibitor; antagonist; integrin alpha-v beta-3;
KW   vitronectin receptor; rheumatoid arthritis; tumour; metastasis;
KW   diabetic retinopathy; macular degeneration; restenosis; therapy;
KW   circular; cyclic.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 4
FT                   /note= "D-form residue"
XX
PN   WO9745137-A1.
XX
PD   04-DEC-1997.
XX
PF   30-MAY-1997;   97WO-US09158.
XX
PR   31-MAY-1996;   96US-0018733.
PR   31-MAY-1996;   96US-0015869.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Brooks P,  Cheresh DA;
XX
DR   WPI; 1998-032334/03.
XX
PT   Packaging material containing polypeptide antagonist of alphav,
PT   beta3 integrin - used for inhibition of angiogenesis, and for
PT   treating tumours, inflammation, eye diseases etc.
XX
PS   Example 1; Page 48; 234pp; English.
XX
CC   This synthetic RGD-containing cyclic peptide, designated 62184 or
CC   65203, is a particularly preferred peptide that has integrin
CC   alpha-v beta-3 antagonist activity.  It exhibits preferential
CC   inhibition of fibrinogen binding to the alpha-v beta-3 receptor.
CC   It can be prepared using standard solid-phase synthesis
CC   techniques.  The invention relates to the discovery that
CC   angiogenesis is mediated by the specific vitronectin receptor
CC   alpha-v beta-3, and that inhibition of alpha-v beta-3 function
CC   inhibits angiogenesis.  Claimed antagonists of alpha-v beta-3
CC   comprise C-terminal fragments (see W41083-94) of human or chicken
CC   matrix metalloproteinase-2, fusion polypeptides, cyclic or linear
CC   polypeptides, derivatised polypeptides, a monoclonal antibody or
CC   organic mimetic compound.  They can be used to inhibit angiogenesis
CC   in inflammed tissue (for treatment of arthritis or rheumatoid
CC   arthritis), in solid tumours or metastases (particularly to induce
CC   regression or inhibit tumour growth), and in ocular disorders such
CC   as diabetic retinopathy and macular degeneration, as well as to
CC   treat restenosis (all claimed).
XX
SQ   Sequence   5 AA;

  Query Match           100.0%;  Score 27;  DB 19;  Length 5;
  Best Local Similarity  100.0%;  Pred. No. 2.1e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

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Qy      1 RGDFV 5
          |||||
Db      1 rgdfv 5
```

```
RESULT  10
W41101
ID   W41101 standard; Peptide; 5 AA.
XX
AC   W41101;
XX
DT   08-JUN-1998  (first entry)
XX
DE   Alpha-v beta-3 antagonist cyclic peptide 62187.
XX
KW   Angiogenesis; inhibitor; antagonist; integrin alpha-v beta-3;
KW   vitronectin receptor; rheumatoid arthritis; tumour; metastasis;
KW   diabetic retinopathy; macular degeneration; restenosis; therapy;
KW   circular; cyclic.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 5
FT                   /note= "D-form residue"
XX
PN   WO9745137-A1.
XX
PD   04-DEC-1997.
XX
PF   30-MAY-1997;   97WO-US09158.
XX
PR   31-MAY-1996;   96US-0018733.
PR   31-MAY-1996;   96US-0015869.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Brooks P,  Cheresh DA;
XX
DR   WPI; 1998-032334/03.
XX
PT   Packaging material containing polypeptide antagonist of alphav,
PT   beta3 integrin - used for inhibition of angiogenesis, and for
PT   treating tumours, inflammation, eye diseases etc.
XX
PS   Example 1; Page 48; 234pp; English.
XX
CC   This synthetic RGD-containing cyclic peptide, designated 62187,
CC   is a particularly preferred peptide that has integrin
CC   alpha-v beta-3 antagonist activity.  It exhibits preferential
CC   inhibition of fibrinogen binding to the alpha-v beta-3 receptor.
CC   It can be prepared using standard solid-phase synthesis
CC   techniques.  The invention relates to the discovery that
CC   angiogenesis is mediated by the specific vitronectin receptor
CC   alpha-v beta-3, and that inhibition of alpha-v beta-3 function
CC   inhibits angiogenesis.  Claimed antagonists of alpha-v beta-3
CC   comprise C-terminal fragments (see W41083-94) of human or chicken
CC   matrix metalloproteinase-2, fusion polypeptides, cyclic or linear
CC   polypeptides, derivatised polypeptides, a monoclonal antibody or
CC   organic mimetic compound.  They can be used to inhibit angiogenesis
CC   in inflammed tissue (for treatment of arthritis or rheumatoid
CC   arthritis), in solid tumours or metastases (particularly to induce
CC   regression or inhibit tumour growth), and in ocular disorders such
CC   as diabetic retinopathy and macular degeneration, as well as to
CC   treat restenosis (all claimed).
XX
SQ   Sequence   5 AA;
```

```
 Query Match           100.0%;  Score 27;  DB 19;  Length 5;
 Best Local Similarity  100.0%;  Pred. No. 2.1e+05;
 Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy      1 RGDFV 5
          |||||
Db      1 rgdfv 5
```

```
RESULT  11
W41109
ID   W41109 standard; Peptide; 5 AA.
XX
AC   W41109;
XX
DT   08-JUN-1998  (first entry)
XX
DE   Alpha-v beta-3 antagonist cyclic peptide 121974 (85189).
XX
KW   Angiogenesis; inhibitor; antagonist; integrin alpha-v beta-3;
KW   vitronectin receptor; rheumatoid arthritis; tumour; metastasis;
KW   diabetic retinopathy; macular degeneration; restenosis; therapy;
KW   circular; cyclic.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   5
FT                   /note= "valine residue NH2 terminal is
FT                         methylated"
XX
PN   WO9745137-A1.
XX
PD   04-DEC-1997.
XX
PF   30-MAY-1997;   97WO-US09158.
XX
PR   31-MAY-1996;   96US-0018733.
PR   31-MAY-1996;   96US-0015869.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Brooks P,  Cheresh DA;
XX
DR   WPI; 1998-032334/03.
XX
PT   Packaging material containing polypeptide antagonist of alphav,
PT   beta3 integrin - used for inhibition of angiogenesis, and for
PT   treating tumours, inflammation, eye diseases etc.
XX
PS   Example 1; Page 51; 234pp; English.
XX
CC   This synthetic RGD-containing cyclic peptide, designated 121974 or
CC   85189, is a particularly preferred peptide that has integrin
CC   alpha-v beta-3 antagonist activity.  It can be prepared using
CC   standard solid-phase synthesis techniques.  The invention relates
CC   to the disccvery that angiogenesis is mediated by the specific
CC   vitronectin receptor alpha-v beta-3, and that inhibition of alpha-v
CC   beta-3 function inhibits angiogenesis.  Claimed antagonists of
CC   alpha-v beta-3 comprise C-terminal fragments (see W41083-94) of
CC   human or chicken matrix metalloproteinase-2, fusion polypeptides,
CC   cyclic or linear polypeptides, derivatised polypeptides, a
CC   monoclonal antibody or organic mimetic compound.  They can be used
CC   to inhibit angiogenesis in inflammed tissue (for treatment of
CC   arthritis or rheumatoid arthritis), in solid tumours or metastases
CC   (particularly to induce regression or inhibit tumour growth), and
CC   in ocular disorders such as diabetic retinopathy and macular
CC   degeneration, as well as to treat restenosis (all claimed).
XX
SQ   Sequence   5 AA;
```

```
 Query Match           100.0%;  Score 27;  DB 19;  Length 5;
 Best Local Similarity  100.0%;  Pred. No. 2.1e+05;
 Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy      1 RGDFV 5
          |||||
Db      1 rgdfv 5


RESULT  12
W41240
ID   W41240 standard; protein; 5 AA.
XX
AC   W41240;
XX
DT   09-JUN-1998  (first entry)
XX
DE   Alpha-v-beta-5 antagonistic peptide 62184.
XX
KW   Alpha-v-beta-5 antagonist; treatment; vitronectin receptor; inhibition;
KW   angiogenesis; tumour growth; restenosis; neovascularisation.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1..5
FT                   /note= "peptide is made cyclic via the first and
FT                         last residues"
FT   Misc-difference 4
FT                   /note= "D-form residue"
XX
PN   WO9745447-A1.
XX
PD   04-DEC-1997.
XX
PF   30-MAY-1997;   97WO-US09099.
XX
PR   31-MAY-1996;   96US-0018733.
PR   31-MAY-1996;   96US-0015869.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Brooks P,  Cheresh DA,  Friedlander M;
XX
DR   WPI; 1998-041758/04.
XX
PT   Packaging material containing polypeptide antagonist of alphav,
PT   beta5 integrin - used for inhibition of angiogenesis, and for
PT   treating tumours, inflammation, eye diseases etc.
XX
PS   Disclosure; Page 41; 117pp; English.
XX
CC   The present peptide represents an alpha-v-beta-5 integrin antagonists.
CC   Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of alpha-v-beta-5
CC   can inhibit angiogenesis. The specification describes a novel
CC   labelled package that contains an inhibitor of angiogenesis i.e. an
CC   alpha-v-beta-5 antagonising polypeptide that binds to integrin
CC   alpha-v-beta-5 and includes a part of the C-terminal domain of MMP-2.
CC   The antagonists are used to inhibit angiogenesis in inflamed tissue, in
CC   solid tumours or metastases, and in a wide range of ocular disorders
CC   (e.g. diabetic or other forms of retinopathy, neovascular glaucoma, or
CC   corneal transplants). They are particularly used to induce regression or
CC   to inhibit growth of tumours. The alpha-v-beta-5 antagonists can also be
CC   used to treat restenosis caused by migration of smooth muscle cells
CC   following angioplasty and to reduce blood supply to selected tissues.
CC   The antagonists particularly inhibit neovascularisation where this is
CC   induced by cytokines, e.g. transforming growth factor alpha, epidermal
CC   growth factor or especially vascular endothelial growth factor.
CC   note: this sequence does not appear in the specification; it was created
CC   using information provided.
XX
SQ   Sequence   5 AA;

 Query Match             100.0%;  Score 27;  DB 19;  Length 5;
 Best Local Similarity   100.0%;  Pred. No. 2.1e+05;
 Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RGDFV 5
          |||||
Db      1 rgdfv 5


RESULT  13
W41243
ID   W41243 standard; protein; 5 AA.
XX
AC   W41243;
XX
DT   09-JUN-1998  (first entry)
XX
DE   Alpha-v-beta-5 antagonistic peptide 62187.
XX
KW   Alpha-v-beta-5 antagonist; treatment; vitronectin receptor; inhibition;
KW   angiogenesis; tumour growth; restenosis; neovascularisation.
XX
OS   Synthetic.
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FH   Key             Location/Qualifiers
FT   Misc-difference 1..5
FT                   /note= "peptide is made cyclic via the first and
FT                         last residues"
FT   Misc-difference 5
FT                   /note= "D-form residue"
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PN   WO9745447-A1.
XX
PD   04-DEC-1997.
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PF   30-MAY-1997;   97WO-US09099.
XX
PR   31-MAY-1996;   96US-0018733.
PR   31-MAY-1996;   96US-0015869.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Brooks P,  Cheresh DA,  Friedlander M;
XX
DR   WPI; 1998-041758/04.
XX
PT   Packaging material containing polypeptide antagonist of alphav,
PT   beta5 integrin - used for inhibition of angiogenesis, and for
PT   treating tumours, inflammation, eye diseases etc.
XX
PS   Disclosure; Page 41; 117pp; English.
XX
CC   The present peptide represents an alpha-v-beta-5 integrin antagonists.
CC   Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of alpha-v-beta-5
CC   can inhibit angiogenesis. The specification describes a novel
CC   labelled package that contains an inhibitor of angiogenesis i.e. an
CC   alpha-v-beta-5 antagonising polypeptide that binds to integrin
CC   alpha-v-beta-5 and includes a part of the C-terminal domain of MMP-2.
CC   The antagonists are used to inhibit angiogenesis in inflamed tissue, in
CC   solid tumours or metastases, and in a wide range of ocular disorders
CC   (e.g. diabetic or other forms of retinopathy, neovascular glaucoma, or
CC   corneal transplants). They are particularly used to induce regression or
CC   to inhibit growth of tumours. The alpha-v-beta-5 antagonists can also be
CC   used to treat restenosis caused by migration of smooth muscle cells
CC   following angioplasty and to reduce blood supply to selected tissues.
CC   The antagonists particularly inhibit neovascularisation where this is
CC   induced by cytokines, e.g. transforming growth factor alpha, epidermal
CC   growth factor or especially vascular endothelial growth factor.
CC   note: this sequence does not appear in the specification; it was created
CC   using information provided.
XX
SQ   Sequence   5 AA;

 Query Match             100.0%;  Score 27;  DB 19;  Length 5;
 Best Local Similarity   100.0%;  Pred. No. 2.1e+05;
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Db      1 rgdfv 5


RESULT  14
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ID   W41247 standard; protein; 5 AA.
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AC   W41247;
XX
DT   09-JUN-1998  (first entry)
XX
DE   Alpha-v-beta-5 antagonistic peptide.
XX
KW   Alpha-v-beta-5 antagonist; treatment; vitronectin receptor; inhibition;
KW   angiogenesis; tumour growth; restenosis; neovascularisation.
XX
OS   Synthetic.
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FH   Key             Location/Qualifiers
FT   Misc-difference 4
FT                   /note= "D-form residue"
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PR   31-MAY-1996;   96US-0015869.
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PI   Brooks P,  Cheresh DA,  Friedlander M;
XX
DR   WPI; 1998-041758/04.
XX
PT   Packaging material containing polypeptide antagonist of alphav,
PT   beta5 integrin - used for inhibition of angiogenesis, and for
PT   treating tumours, inflammation, eye diseases etc.
XX
PS   Disclosure; Page 38; 117pp; English.
XX
CC   The present peptide represents an alpha-v-beta-5 integrin antagonists.
CC   Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of alpha-v-beta-5
CC   can inhibit angiogenesis. The specification describes a novel
CC   labelled package that contains an inhibitor of angiogenesis i.e. an
CC   alpha-v-beta-5 antagonising polypeptide that binds to integrin
CC   alpha-v-beta-5 and includes a part of the C-terminal domain of MMP-2.
CC   The antagonists are used to inhibit angiogenesis in inflamed tissue, in
CC   solid tumours or metastases, and in a wide range of ocular disorders
CC   (e.g. diabetic or other forms of retinopathy, neovascular glaucoma, or
CC   corneal transplants). They are particularly used to induce regression or
CC   to inhibit growth of tumours. The alpha-v-beta-5 antagonists can also be
CC   used to treat restenosis caused by migration of smooth muscle cells
CC   following angioplasty and to reduce blood supply to selected tissues.
CC   The antagonists particularly inhibit neovascularisation where this is
CC   induced by cytokines, e.g. transforming growth factor alpha, epidermal
CC   growth factor or especially vascular endothelial growth factor.
CC   note: this sequence does not appear in the specification; it was created
CC   using information provided.
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SQ   Sequence   5 AA;


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Qy      1 RGDFV 5
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Db      1 rgdfv 5


RESULT  15
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ID   W92307 standard; peptide; 5 AA.
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AC   W92307;
XX
DT   01-APR-1999  (first entry)
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DE   Cyclic azapeptide #1.
XX
KW   Cyclic peptide; azapeptide; integrin inhibitor; treatment; thrombosis;
KW   cardiac infarct; coronary heart disease; arteriosclerosis; tumour;
KW   osteoporosis; inflammation; infection; angiogenesis; antimicrobial;
KW   diagnosis; platelet metabolism; fibrinogen receptor; cancer; metastasis;
KW   intracellular signalling; GpIIb/IIIa receptor; matrix metalloproteinase;
KW   vitronectin receptor.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1..5
FT                   /note= "The carboxy group of Val(5) is condensed onto
FT                           the amino group of Arg(1) to form a cyclic
FT                           peptide. Not true N- and C- terminus.
FT                           Val(5) can be modified by N-Me"
FT   Modified-site   2
FT                   /note= "aza-Gly"
FT   Misc-difference 4
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PN   DE19728524-A1.
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PD   07-JAN-1999.
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PF   04-JUL-1997;   97DE-1028524.
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PR   04-JUL-1997;   97DE-1028524.
XX
PA   (MERE ) MERCK PATENT GMBH.
XX
PI   Goodman SL,  Jonczyk A,  Kessler H,  Schmitt J,  Wermuth J;
XX
DR   WPI; 1999-072017/07.
XX
PT   New cyclic pentapeptide(s) containing aza-amino acid - are
PT   inhibitors of integrin-ligand interaction, used to treat e.g.
PT   thrombosis, cardiac infarct, coronary heart disease and tumours
XX
PS   Claim 3a; Page 11; 12pp; German.
XX
CC   This invention is concerned with novel cyclic peptides of formula
CC   cyclo(aArg-aGly-aAsp-aX-aY) where aArg = Arg or aza-Arg, aGly = Gly or
CC   aza-Gly, aAsp = Asp or aza-Asp, aX, aY = Ala, Asn, Asp, Arg, Cys, Gln,
CC   Glu, Gly, His, Ile, Leu, Lys, Met, Nle (norleucine), Orn (ornithine),
CC   Phe, Phg (phenylglycine), Pro, Ser, Thr, Tic (tetrahydroisoquinoline-
CC   3-carboxylic acid), Trp, Tyr, Val or NH-Q-CO, or the corresponding
CC   aza-amino acids, Q = 1-6C alkylene, at least one amino acid (aa) in the
CC   peptide has the alpha-carbon atom replaced by nitrogen also the aa may
CC   be derivatised and are coupled together by peptide bonds and optically
CC   active amino acids may be in D- or L-forms. The peptides are integrin
CC   inhibitors, specifically for treating and preventing thrombosis, cardiac
CC   infarct, coronary heart disease, arteriosclerosis, tumours, osteoporosis,
CC   inflammation and infections, or generally any disease where angiogenesis
CC   is involved, in human or veterinary medicine. The peptides also have
CC   antimicrobial activity, are used for diagnosis and location of thrombi,
CC   and for studying metabolism of platelets at different stages of
```

CC activation or intracellular signalling mechanisms of the fibrinogen
CC receptor, and for affinity purification of integrins. The peptides
CC inhibit interaction between the alpha v, beta 3 and beta 5 receptors with
CC their ligands, e.g. they prevent binding of fibrinogen to the GpIIb/IIIa
CC receptor, thus preventing metastatic spread of cancers, and prevent
CC binding of matrix metalloproteinase to the vitronectin (alpha v beta 3)
CC receptor. This sequence is a specific claimed example of a novel peptide
CC of the invention.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 27; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGDFV 5
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Search completed: March 6, 2001, 09:45:52
Job time: 58 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: March 6, 2001, 09:45:18 ; Search time 19.1 Seconds
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Title: US-09-081-522-7
Perfect score: 27
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Scoring table: BLOSUM62
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Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 14061

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	27	100.0	5	1	US-08-210-715-7	Sequence 7, Appli
3	27	100.0	5	1	US-08-366-665-5	Sequence 5, Appli
4	27	100.0	5	1	US-08-366-665-7	Sequence 7, Appli
5	27	100.0	5	2	US-08-616-770-2	Sequence 2, Appli
6	23	85.2	4	1	US-07-932-200-10	Sequence 10, Appl
7	23	85.2	4	1	US-08-596-116A-68	Sequence 68, Appl
8	23	85.2	4	2	US-08-668-871-12	Sequence 12, Appl
9	23	85.2	4	2	US-08-669-683-12	Sequence 12, Appl
10	23	85.2	4	2	US-08-387-749-10	Sequence 10, Appl
11	23	85.2	4	2	US-08-335-832-25	Sequence 25, Appl
12	23	85.2	4	2	US-08-753-781-20	Sequence 20, Appl
13	23	85.2	4	2	US-08-361-864-28	Sequence 28, Appl
14	23	85.2	4	4	PCT-US93-08231-10	Sequence 10, Appl
15	23	85.2	4	5	5330911-12	Patent No. 5330911
16	23	85.2	5	1	US-08-315-026B-10	Sequence 10, Appl
17	23	85.2	5	2	US-08-616-770-1	Sequence 1, Appli
18	23	85.2	5	2	US-08-754-773B-10	Sequence 10, Appl
19	23	85.2	5	3	US-09-141-127-23	Sequence 23, Appl
20	23	85.2	5	3	US-09-155-721-1	Sequence 1, Appli
21	23	85.2	5	3	US-09-155-721-2	Sequence 2, Appli
22	23	85.2	5	3	US-09-155-721-4	Sequence 4, Appli
23	23	85.2	5	3	US-09-155-721-5	Sequence 5, Appli
24	23	85.2	5	3	US-09-155-721-6	Sequence 6, Appli
25	23	85.2	5	3	US-09-155-721-7	Sequence 7, Appli
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29	22	81.5	5	3	US-08-694-387A-22	Sequence 22, Appl
30	22	81.5	5	3	US-08-694-387A-23	Sequence 23, Appl
31	22	81.5	5	3	US-08-694-387A-24	Sequence 24, Appl
32	22	81.5	5	3	US-08-694-387A-25	Sequence 25, Appl
33	22	81.5	5	3	US-08-694-387A-27	Sequence 27, Appl
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35	22	81.5	5	3	US-08-694-387A-30	Sequence 30, Appl
36	22	81.5	5	3	US-08-694-387A-32	Sequence 32, Appl
37	22	81.5	5	3	US-08-694-387A-33	Sequence 33, Appl
38	22	81.5	5	3	US-08-694-387A-34	Sequence 34, Appl
39	22	81.5	5	3	US-08-694-387A-35	Sequence 35, Appl
40	22	81.5	5	3	US-08-694-387A-37	Sequence 37, Appl
41	22	81.5	5	3	US-08-694-387A-38	Sequence 38, Appl
42	22	81.5	5	3	US-08-694-387A-39	Sequence 39, Appl
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ALIGNMENTS

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RESULT 1
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; Patent No. 5753230
; GENERAL INFORMATION:
;   APPLICANT: Brooks, Peter
;   APPLICANT: Cheresh, David A
;   TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR
;   TITLE OF INVENTION: INHIBITION OF ANGIOGENESIS
;   NUMBER OF SEQUENCES: 14
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Office of Patent Counsel, The Scripps
;     ADDRESSEE: Research Institute
;     STREET: 10665 No. 5753230th Torrey Pines Road, TPC-8
;     CITY: La Jolla
;     STATE: CA
;     COUNTRY: USA
;     ZIP: 92037
;   COMPUTER READABLE FORM:
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;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/210,715
;     FILING DATE: 18-MAR-1994
;     CLASSIFICATION: 514
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Fitting, Thomas
;     REGISTRATION NUMBER: 34,163
;     REFERENCE/DOCKET NUMBER: TSRI 419.0
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (619) 554-2937
;     TELEFAX: (619) 554-6312
; INFORMATION FOR SEQ ID NO: 5:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 5 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: circular
;   MOLECULE TYPE: peptide
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
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;     NAME/KEY: Peptide
;     LOCATION: 1..5
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;     OTHER INFORMATION: /note= "Cyclo signifies a cyclic peptide; lower
;     OTHER INFORMATION: case letters indicate a D-amino acid; capital
;     OTHER INFORMATION: letters indicate a L-amino acid."
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US-08-210-715-5

Query Match 100.0%; Score 27; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 RGDFV 5

RESULT 2
US-08-210-715-7
; Sequence 7, Application US/08210715
; Patent No. 5753230
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheresh, David A
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR
; TITLE OF INVENTION: INHIBITION OF ANGIOGENESIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 No. 5753230th Torrey Pines Road, TPC-8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/210,715
; FILING DATE: 18-MAR-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 419.0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 554-2937
; TELEFAX: (619) 554-6312
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
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; NAME/KEY: Peptide
; LOCATION: 1..5
; OTHER INFORMATION: /label= cyclo
; OTHER INFORMATION: /note= "Cyclo signifies a cyclic peptide; lower
; OTHER INFORMATION: case letters indicate a D-amino acid; capital
; OTHER INFORMATION: letters indicate a L-amino acid."
US-08-210-715-7

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Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 RGDFV 5

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; Sequence 5, Application US/08366665
; Patent No. 5766591
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheresh, David A
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR
; TITLE OF INVENTION: INHIBITION OF ANGIOGENESIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 No. 5766591th Torrey Pines Road, TPC-8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
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; APPLICATION NUMBER: US/08/366,665
; FILING DATE: 30-DEC-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/210,715
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 419.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 554-2937
; TELEFAX: (619) 554-6312
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
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; OTHER INFORMATION: letters indicate a L-amino acid."
US-08-366-665-5

Query Match 100.0%; Score 27; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGDFV 5
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Db 1 RGDFV 5

RESULT 4
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; Patent No. 5766591
; GENERAL INFORMATION:

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;    APPLICANT:  Brooks, Peter
;    APPLICANT:  Cheresh, David A
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS USEFUL FOR
;    TITLE OF INVENTION:  INHIBITION OF ANGIOGENESIS
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Office of Patent Counsel, The Scripps
;      ADDRESSEE:  Research Institute
;      STREET:  10666 No. 5766591th Torrey Pines Road, TPC-8
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
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;      CLASSIFICATION:  424
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;      FILING DATE:  18-MAR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fitting, Thomas
;      REGISTRATION NUMBER:  34,163
;      REFERENCE/DOCKET NUMBER:  TSRI 419.1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 554-2937
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;      OTHER INFORMATION:  letters indicate a L-amino acid."
US-08-366-665-7


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Db      1 RGDFV 5


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;  GENERAL INFORMATION:
;    APPLICANT:  Jonczyk, Alfred
;    APPLICANT:  Holzemann, Gunter
;    APPLICANT:  Felding-Habermann, Brunhilde
;    APPLICANT:  Rippmann, Friedrich
;    APPLICANT:  Diefenbach, Beate
;    APPLICANT:  Kessler, Horst
;    APPLICANT:  Haubner, Roland
;    APPLICANT:  Wermuth, Jochen
;    TITLE OF INVENTION:  Cyclic Peptides Containing Arg-Gly-Asp, and
;    TITLE OF INVENTION:  Derivatives Thereof, as Adhesion Inhibitors
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Millen, White, Zelano & Branigan, P.C.
;      STREET:  2200 Clarendon Boulevard, Suite 1400
;      CITY:  Arlington
;      STATE:  VA
;      COUNTRY:  U.S.A.
;      ZIP:  22201
;    COMPUTER READABLE FORM:
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;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/220,858
;      FILING DATE:  31-MAR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DE P 43 10 643.9
;      FILING DATE:  01-APR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Heaney, Brion P.
;      REGISTRATION NUMBER:  32,542
;      REFERENCE/DOCKET NUMBER:  MERCK 1566C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-243-6333
;      TELEFAX:  703-243-6410
;      TELEX:  64191
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  peptide
US-08-616-770-2


  Query Match             100.0%;  Score 27;  DB 2;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RGDFV 5
          |||||
Db      1 RGDFV 5


RESULT  6
US-07-932-200-10
; Sequence 10, Application US/07932200
; Patent No. 5366862
;  GENERAL INFORMATION:
;    APPLICANT:  VENTON, DUANE L.
;    APPLICANT:  HOPFINGER, ANTON J.
;    APPLICANT:  LE BRETON, GUY
;    TITLE OF INVENTION:  METHOD FOR GENERATING AND SCREENING
;    TITLE OF INVENTION:  USEFUL PEPTIDES
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 SEVENTH STREET, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
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;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/932,200
;      FILING DATE:  21-AUG-1992
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  COOPER, IVER P.
;      REGISTRATION NUMBER:  28,005
;      REFERENCE/DOCKET NUMBER:  VENTON=1B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;      TELEX:  248633
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-07-932-200-10


  Query Match             85.2%;  Score 23;  DB 1;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RGDF 4
          ||||
Db      1 RGDF 4


RESULT   7
US-08-596-116A-68
; Sequence 68, Application US/08596116A
; Patent No. 5721213
;  GENERAL INFORMATION:
;    APPLICANT:  SATO, Yoshimi
;    APPLICANT:  HAYASHI, Yoshio
;    APPLICANT:  KATADA, Jun
;    TITLE OF INVENTION:  No. 5721213el Peptides, Active as Inhibitors of
;    TITLE OF INVENTION:  Platelet Aggregation
;    NUMBER OF SEQUENCES:  71
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Kenyon & Kenyon
;      STREET:  1025 Connecticut Avenue, N.W., Suite 600
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3+ Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS 6.2
;      SOFTWARE:  WordPerfect 6.1 for Windows
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/596,116A
;      FILING DATE:  30 JAN 1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP94/01611
;      FILING DATE:  29 SEP 1994
;      APPLICATION NUMBER:  JP 245541
;      FILING DATE:  30 SEP 1993
;      APPLICATION NUMBER:  JP 50602
;      FILING DATE:  22 MAR 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Toffenetti, Judith L.
;      REGISTRATION NUMBER:  39,048
;      REFERENCE/DOCKET NUMBER:  2002/3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-429-1776
;      TELEFAX:  202-429-0796
;  INFORMATION FOR SEQ ID NO:  68:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-596-116A-68


  Query Match             85.2%;  Score 23;  DB 1;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RGDF 4
          ||||
Db      1 RGDF 4


RESULT   8
US-08-668-871-12
; Sequence 12, Application US/08668871
; Patent No. 5811389
;  GENERAL INFORMATION:
;    APPLICANT:  Bannwarth, Wilhelm
;    APPLICANT:  Gerber, Fernand
;    APPLICANT:  Grieder, Alfred
;    APPLICANT:  Knierzinger, Andreas
;    APPLICANT:  Mueller, Klaus
;    APPLICANT:  Obrecht, Daniel
;    APPLICANT:  Trzeciak, Arnold
;    TITLE OF INVENTION:  TRI- AND TETRACYCLIC COMPOUNDS
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  United States of America
;      ZIP:  07110-1199
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/668,871
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/106,508
;      FILING DATE:
;      APPLICATION NUMBER:  CH 2725/92
;      FILING DATE:  31-AUG-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kass, Alan P
;      REGISTRATION NUMBER:  32142
;      REFERENCE/DOCKET NUMBER:  RAN 4781/1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 235-4205
;      TELEFAX:  (201) 235-3500
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-668-871-12


  Query Match             85.2%;  Score 23;  DB 2;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy      1 RGDF 4
          ||||
Db      1 RGDF 4


RESULT   9
US-08-669-683-12
; Sequence 12, Application US/08669683
; Patent No. 5811548
;  GENERAL INFORMATION:
;    APPLICANT:  Bannwarth, Wilhelm
;    APPLICANT:  Gerber, Fernand
;    APPLICANT:  Grieder, Alfred
;    APPLICANT:  Knierzinger, Andreas
;    APPLICANT:  Mueller, Klaus
;    APPLICANT:  Obrecht, Daniel
;    APPLICANT:  Trzeciak, Arnold
;    TITLE OF INVENTION:  TRI- AND TETRACYCLIC COMPOUNDS
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  United States of America
;      ZIP:  07110-1199
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/569,683
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/106,508
;      FILING DATE:
;      APPLICATION NUMBER:  CH 2725/92
;      FILING DATE:  31-AUG-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kass, Alan P
;      REGISTRATION NUMBER:  32142
;      REFERENCE/DOCKET NUMBER:  RAN 4781/1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 235-4205
;      TELEFAX:  (201) 235-3500
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-669-683-12


  Query Match           85.2%;  Score 23;  DB 2;  Length 4;
  Best Local Similarity  100.0%;  Pred. No. 1.3e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RGDF 4
          ||||
Db      1 RGDF 4


RESULT  10
US-08-387-749-10
; Sequence 10, Application US/08387749
; Patent No. 5814460
;  GENERAL INFORMATION:
;    APPLICANT:  VENTON, DUANE L.
;    APPLICANT:  HOFFINGER, ANTON J.
;    APPLICANT:  LE BRETON, GUY
;    TITLE OF INVENTION:  METHOD FOR GENERATING AND SCREENING
;    TITLE OF INVENTION:  USEFUL PEPTIDES
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 SEVENTH STREET, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/387,749
;      FILING DATE:  21-Feb-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/08231
;      FILING DATE:  09-AUG-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/932,200
;      FILING DATE:  21-AUG-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/813,315
;      FILING DATE:  21-AUG-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US91/00891
;      FILING DATE:  14-FEB-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/480,865
;      FILING DATE:  14-FEB-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  COOPER, IVER P.
;      REGISTRATION NUMBER:  28,005
;      REFERENCE/DOCKET NUMBER:  VENTON-1C
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;      TELEX:  248633
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-387-749-10


  Query Match           85.2%;  Score 23;  DB 2;  Length 4;
  Best Local Similarity  100.0%;  Pred. No. 1.3e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RGDF 4
          ||||
Db      1 RGDF 4


RESULT  11
US-08-335-832-25
; Sequence 25, Application US/08335832
; Patent No. 5925331
;  GENERAL INFORMATION:
;    APPLICANT:  Dean, Richard T
;    APPLICANT:  Lister-James, John
;    TITLE OF INVENTION:  Technetium-99m Labeled Peptides for
;    TITLE OF INVENTION:  Thrombus Imaging
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
```

```
;       ADDRESSEE:  Banner & Allegretti, Ltd.
;       STREET:  10 South Wacker Drive Suite 3000
;       CITY:  Chicago
;       STATE:  Illinois
;       COUNTRY:  USA
;       ZIP:  60606
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/335,832
;       FILING DATE:  05-JAN-1995
;       CLASSIFICATION:  424
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  No. 5925331nan, Kevin E
;       REGISTRATION NUMBER:  35,303
;       REFERENCE/DOCKET NUMBER:  92,216-I
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  312-715-1000
;       TELEFAX:  312-715-1234
;       TELEX:  910-221-5317
;   INFORMATION FOR SEQ ID NO:  25:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  4 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  1
;       OTHER INFORMATION:  /label= ma
;       OTHER INFORMATION:  /note= "The amino terminus is modified by covalent
;       OTHER INFORMATION:  linkage to an mercaptoacetyl group."
US-08-335-832-25


  Query Match             85.2%;  Score 23;  DB 2;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RGDF 4
          ||||
Db      1 RGDF 4


RESULT  12
US-08-753-781-20
; Sequence 20, Application US/08753781C
; Patent No. 5951981
; GENERAL INFORMATION:
;  APPLICANT: Markland Jr., Francis S.
;  APPLICANT: Bush, Larry R.
;  APPLICANT: Swenson, Stephen
;  APPLICANT: Flores Sanchez, Eladio
;  TITLE OF INVENTION: THROMBOLYTIC AGENTS WITH ANTITHROMBOTIC ACTIVITY
;  FILE REFERENCE: DITI 124
;  CURRENT APPLICATION NUMBER: US/08/753,781C
;  CURRENT FILING DATE: 1996-12-02
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
;   LENGTH: 4
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (1)
;   OTHER INFORMATION: meercaptoacetyl
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:synthetic
;   OTHER INFORMATION: peptide
US-08-753-781-20


  Query Match             85.2%;  Score 23;  DB 2;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RGDF 4
          ||||
Db      1 RGDF 4


RESULT  13
US-08-361-864-28
; Sequence 28, Application US/08361864
; Patent No. 5977064
; GENERAL INFORMATION:
;   APPLICANT:  Dean, Richard T
;   APPLICANT:  Lister-James, John
;   TITLE OF INVENTION:  Multimeric Polyvalent Antithrombotic
;   TITLE OF INVENTION:  Agents
;   NUMBER OF SEQUENCES:  37
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Allegretti & Witcoff, Ltd.
;     STREET:  10 South Wacker Drive, Suite 3000
;     CITY:  Chicago
;     STATE:  Illinois
;     COUNTRY:  USA
;     ZIP:  60606
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/361,864
;     FILING DATE:
;     CLASSIFICATION:  514
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US/07/955,466A
;     FILING DATE:  19921002
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  No. 5977064nan, Kevin E
;     REGISTRATION NUMBER:  35,303
;     REFERENCE/DOCKET NUMBER:  92,668
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  312-715-1000
;     TELEFAX:  312-715-1234
;     TELEX:  910-221-5317
;  INFORMATION FOR SEQ ID NO:  28:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  4 amino acids
;     TYPE:  amino acid
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  peptide
US-08-361-864-28


  Query Match             85.2%;  Score 23;  DB 2;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RGDF 4
          ||||
Db      1 RGDF 4


RESULT  14
PCT-US93-08231-10
; Sequence 10, Application PC/TUS9308231
;  GENERAL INFORMATION:
;    APPLICANT:  VENTON, DUANE L.
;    APPLICANT:  HOPFINGER, ANTON J.
```

```
;    APPLICANT:  LE BRETON, GUY
;    TITLE OF INVENTION:  METHOD FOR GENERATING AND SCREENING
;    TITLE OF INVENTION:  USEFUL PEPTIDES
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 SEVENTH STREET, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/08231
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  COOPER, IVER P.
;      REGISTRATION NUMBER:  28,005
;      REFERENCE/DOCKET NUMBER:  VENTON1C.PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;      TELEX:  248633
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
PCT-US93-08231-10


  Query Match             85.2%;  Score 23;  DB 4;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RGDF 4
          ||||
Db      1 RGDF 4


RESULT  15
5330911-12
;Patent No. 5330911
;    APPLICANT: HUBBELL, JEFFREY A.;MASSIA, STEPHEN P.;DESAI,
;NEIL P.
;    TITLE OF INVENTION: SURFACES HAVING DESIRABLE CELL
;ADHESIVE EFFECTS
;    NUMBER OF SEQUENCES: 27
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/527,198
;      FILING DATE: 21-MAY-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 414,144
;      FILING DATE: 28-SEP-1989
;SEQ ID NO:12:
;      LENGTH: 4
5330911-12


  Query Match             85.2%;  Score 23;  DB 5;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RGDF 4
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Db      1 RGDF 4
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Search completed: March 6, 2001, 09:45:18
Job time: 25 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: March 6, 2001, 09:47:29 ; Search time 20.46 Seconds
(without alignments)
16.594 Million cell updates/sec

Title: US-09-081-522-7
Perfect score: 27
Sequence: 1 RGDFV 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 205

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_66:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	12	44.4	4	2	PT0711	T-cell receptor be
2	12	44.4	5	2	A32516	cholecystokinin-5
3	12	44.4	5	2	PQ0689	photosystem I 10.4
4	12	44.4	5	2	A44692	fulicin - giant Af
5	12	44.4	5	2	B61445	Leu-enkephalin - b
6	12	44.4	5	2	A61445	Met-enkephalin - b
7	12	44.4	5	2	PT0513	T-cell receptor be
8	12	44.4	5	2	PT0538	T-cell receptor be
9	12	44.4	5	2	PT0703	T-cell receptor be
10	12	44.4	5	2	PT0690	T-cell receptor be
11	12	44.4	5	2	PT0573	T-cell receptor be
12	12	44.4	5	2	PT0679	T-cell receptor be
13	11	40.7	4	1	ECXAA	antho-RFamide neur
14	11	40.7	4	2	A25844	autho-RF amide neu
15	11	40.7	4	2	S39390	myosin-light-chain
16	11	40.7	4	2	S47552	ubiquitin - rat
17	11	40.7	5	2	B61168	cocoonase (EC 3.4.
18	11	40.7	5	2	PT0525	T-cell receptor be
19	11	40.7	5	2	PT0608	T-cell receptor be
20	11	40.7	5	2	PT0695	T-cell receptor be
21	11	40.7	5	2	PT0700	T-cell receptor be
22	9	33.3	5	2	S68326	blood cell protein
23	9	33.3	5	4	A58728	serrawettin W2 - S
24	8	29.6	4	2	D41654	hypothetical prote
25	8	29.6	4	2	PT0677	T-cell receptor be
26	8	29.6	5	2	A32014	traM protein - Esc
27	8	29.6	5	2	B45525	actin I - malaria
28	8	29.6	5	2	PT0540	T-cell receptor be
29	7	25.9	3	2	A23751	spinal cord peptid
30	7	25.9	4	2	ECNK	cardioexcitatory n
31	7	25.9	4	2	S09478	globulin IV alpha
32	7	25.9	4	2	A35779	neuropeptide Antho
33	7	25.9	4	2	A60418	FMRFamide - polych
34	7	25.9	4	2	B53284	T-cell receptor be
35	7	25.9	5	2	PT0308	Ig heavy chain CRD
36	7	25.9	5	2	PT0729	T-cell receptor be
37	6	22.2	3	2	GKHU	growth-modulating
38	6	22.2	3	2	A60898	bursin - chicken
39	6	22.2	3	2	B23751	spinal cord peptid
40	6	22.2	3	2	PT0636	T-cell receptor be
41	6	22.2	3	2	PT0571	T-cell receptor be
42	6	22.2	3	2	S68328	blood cell protein
43	6	22.2	4	2	A32039	tyrosine-melanocyt
44	6	22.2	4	2	PL0140	carbon-monoxide de
45	6	22.2	4	2	A25209	protein-glutamine

ALIGNMENTS

RESULT 1
PT0711
T-cell receptor beta chain V-D-J region (120-2J) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0607; PT0674; PT0678; PT0570; PT0711; PT0710
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A;Reference number: PT0509; MUID:91277601
A;Accession: PT0607
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-4 <FE1>
A;Experimental source: newborn thymus, strain BALB/c, 120-2J
A;Accession: PT0674
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-4 <FE2>
A;Experimental source: day 18 fetal thymus, strain BALB/c, 140-1G
A;Accession: PT0678
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-4 <FE3>
A;Experimental source: day 18 fetal thymus, strain BALB/c, 154-1L
A;Accession: PT0570
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-4 <FE4>
A;Experimental source: day 19 fetal thymus, strain BALB/c, 141-1I
A;Accession: PT0711
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-4 <FE5>
A;Experimental source: newborn thymus, strain BALB/c (clones 161-2AE and 161-2AF)
C;Keywords: T-cell receptor

Query Match 44.4%; Score 12; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      2 GD 3
          ||
Db      3 GD 4
```

RESULT 2
A32516
cholecystokinin-5 - dog
N;Alternate names: CCK-5
C;Species: Canis lupus familiaris (dog)

C;Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 18-Aug-2000
C;Accession: A32516
R;Shively, J.; Reeve Jr., J.R.; Eysselein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, J.H.
Am. J. Physiol. 252, G272-G275, 1987
A;Title: CCK-5: sequence analysis of a small cholecystokinin from canine brain and intes
A;Reference number: A32516; MUID:87153871
A;Accession: A32516
A;Molecule type: protein
A;Residues: 1-5 <SHI>
C;Comment: This peptide corresponds to the five carboxyl-terminal residues of cholecysto
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; neuropeptide
F;5/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 44.4%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DF 4
||
Db 4 DF 5

RESULT 3
PQ0689
photosystem I 10.4K H1 chain - common tobacco (fragment)
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 17-Mar-1999
C;Accession: PQ0689
R;Obokata, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugiura, M.
Plant Physiol. 102, 1259-1267, 1993
A;Title: Molecular heterogeneity of photosystem I. psaD, psaE, psaF, psaH and psaL are a
A;Reference number: PQ0667; MUID:94105345
A;Accession: PQ0689
A;Molecule type: protein
A;Residues: 1-5 <OBO>
C;Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match 44.4%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GD 3
||
Db 3 GD 4

RESULT 4
A44692
fulicin - giant African snail
C;Species: Achatina fulica (giant African snail)
C;Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 11-Jul-1997
C;Accession: A44692
R;Ohta, N.; Kubota, I.; Takao, T.; Shimonishi, Y.; Yasuda-Kamatani, Y.; Minakata, H.; No
Biochem. Biophys. Res. Commun. 178, 486-493, 1991
A;Title: Fulicin, a novel neuropeptide containing a D-amino acid residue isolated from t
A;Reference number: A44692; MUID:91315471
A;Accession: A44692
A;Molecule type: protein
A;Residues: 1-5 <OHT>
C;Keywords: amidated carboxyl end; D-amino acid; neuropeptide
F;2/Modified site: D-asparagine (Asn) #status experimental
F;5/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 44.4%; Score 12; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DFV 5
:||
Db 3 EFV 5

RESULT 5
B61445
Leu-enkephalin - blue mussel
C;Species: Mytilus edulis (blue mussel)
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 21-Jan-2000
C;Accession: B61445
R;Leung, M.K.; Stefano, G.B.
Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984
A;Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edu
A;Reference number: A61445; MUID:84144823
A;Accession: B61445
A;Molecule type: protein
A;Residues: 1-5 <LEU>
A;Experimental source: pedal ganglia
C;Keywords: neuropeptide; opioid peptide

Query Match 44.4%; Score 12; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GDFV 5
| |:
Db 2 GGFL 5

RESULT 6
A61445
Met-enkephalin - blue mussel
C;Species: Mytilus edulis (blue mussel)
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 21-Jan-2000
C;Accession: A61445
R;Leung, M.K.; Stefano, G.B.
Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984
A;Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edul
A;Reference number: A61445; MUID:84144823
A;Accession: A61445
A;Molecule type: protein
A;Residues: 1-5 <LEU>
A;Experimental source: pedal ganglia
C;Keywords: neuropeptide; opioid peptide

Query Match 44.4%; Score 12; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GDFV 5
| |:
Db 2 GGFM 5

RESULT 7
PT0513
T-cell receptor beta chain V-D-J region (100-4AL) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0513; PT0606
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A;Reference number: PT0509; MUID:91277601
A;Accession: PT0513
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <FEE>
A;Experimental source: adult thymus, strain BALB/c, clone 100-4AL
A;Accession: PT0506
A;Status: translation not shown
A;Molecule type: mRNA

A;Residues: 1-5 <FE2>
A;Experimental source: newborn thymus, strain BALB/c, clone 120-1S
C;Keywords: T-cell receptor

Query Match 44.4%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GD 3
||
Db 3 GD 4

RESULT 8
PT0538
T-cell receptor beta chain V-D-J region (126-1F) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0538; PT0539; PT0603
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601
A;Accession: PT0538
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <FEE>
A;Experimental source: day 18 fetal thymus, strain BALB/c, clone 126-1F
A;Accession: PT0539
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <FE3>
A;Experimental source: day 18 fetal thymus, strain BALB/c, clone 126-1H
A;Accession: PT0603
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <FE2>
A;Experimental source: newborn thymus, strain BALB/c, clone 100-2AC
C;Keywords: T-cell receptor

Query Match 44.4%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GD 3
||
Db 3 GD 4

RESULT 9
PT0703
T-cell receptor beta chain V-D-J region (135-1F) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0703
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601
A;Accession: PT0703
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-5 <FEE>
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 44.4%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GD 3
||
Db 3 GD 4

RESULT 10
PT0690
T-cell receptor beta chain V-D-J region (140-1BD) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0690
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A;Reference number: PT0509; MUID:91277601
A;Accession: PT0690
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-5 <FEE>
A;Experimental source: day 18 fetal thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 44.4%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GD 3
||
Db 3 GD 4

RESULT 11
PT0573
T-cell receptor beta chain V-D-J region (141-1CC) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0573
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A;Reference number: PT0509; MUID:91277601
A;Accession: PT0573
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <FEE>
A;Experimental source: day 19 fetal thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 44.4%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GD 3
||
Db 3 GD 4

RESULT 12
PT0679
T-cell receptor beta chain V-D-J region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0679; PT0708
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A;Reference number: PT0509; MUID:91277601
A;Accession: PT0679
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-5 <FEE>

A;Experimental source: day 18 fetal thymus, strain BALB/c, 154-2J
A;Accession: PT0708
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-5 <FE2>
A;Experimental source: newborn thymus, strain BALB/c, 161-2B
C;Keywords: T-cell receptor

Query Match 44.4%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GD 3
||
Db 3 GD 4

RESULT 13
ECXAA
antho-RFamide neuropeptide - sea anemone (Anthopleura elegantissima)
C;Species: Anthopleura elegantissima
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 08-Dec-1995
C;Accession: A26666
R;Grimmelikhuijzen, C.J.P.; Graff, D.
Proc. Natl. Acad. Sci. U.S.A. 83, 9817-9821, 1986
A;Title: Isolation of <Glu-Gly-Arg-Phe-NH2 (Antho-RFamide), a neuropeptide from sea anem
A;Reference number: A26666; MUID:87092339
A;Accession: A26666
A;Molecule type: protein
A;Residues: 1-4 <GRI>
C;Comment: The function of this peptide is not known but it could act as a transmitter a
C;Comment: Synthetic and natural peptides had identical properties.
C;Superfamily: RFamide neuropeptide
C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;4/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 40.7%; Score 11; DB 1; Length 4;
Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RGDF 4
:| |
Db 1 QGRF 4

RESULT 14
A25844
autho-RF amide neuropeptide - sea pansy (Renilla koellikeri)
C;Species: Renilla koellikeri (Koelliker's sea pansy)
C;Date: 21-May-1988 #sequence_revision 30-Sep-1993 #text_change 11-Jul-1997
C;Accession: A25844
R;Grimmelikhuijzen, C.J.P.; Groeger, A.
FEBS Lett. 211, 105-108, 1987
A;Title: Isolation of the neuropeptide pGlu-Gly-Arg-Phe-amide from the pennatulid Renill
A;Reference number: A25844
A;Accession: A25844
A;Molecule type: protein
A;Residues: 1-4 <GRI>
C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;4/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 40.7%; Score 11; DB 2; Length 4;
Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RGDF 4
:| |
Db 1 QGRF 4

RESULT 15
S39390
myosin-light-chain kinase (EC 2.7.1.117), smooth muscle - turkey (fragment)
C;Species: Meleagris gallopavo (common turkey)
C;Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 07-May-1999
C;Accession: S39390
R;Komatsu, H.; Ikebe, M.
Biochem. J. 296, 53-58, 1993
A;Title: Affinity labelling of smooth-muscle myosin light-chain kinase with 5'-[p-(f
A;Reference number: S39390; MUID:94071841
A;Accession: S39390
A;Molecule type: protein
A;Residues: 1-4 <KOM>
A;Experimental source: gizzard
C;Keywords: phosphotransferase; smooth muscle

Query Match 40.7%; Score 11; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 2e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GDF 4
| |
Db 2 GKF 4

Search completed: March 6, 2001, 09:47:29
Job time: 155 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: March 6, 2001, 09:48:22 ; Search time 12.72 Seconds
(without alignments)
12.694 Million cell updates/sec

Title: US-09-081-522-7
Perfect score: 27
Sequence: 1 RGDFV 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 28

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	12	44.4	5	1	UXA4_CHLTR	P38005 chlamydia t
2	10	37.0	5	1	TPIS_CANFA	P54714 canis famil
3	9	33.3	5	1	PAP2_PARMA	P81864 pardachirus
4	8	29.6	5	1	TRM3_ECOLI	P13973 escherichia
5	7	25.9	4	1	FLRF_HIRME	P42561 hirudo medi
6	7	25.9	4	1	FMRF_MACNI	P01162 macrocallis
7	6	22.2	3	1	GRWM_HUMAN	P01157 homo sapien
8	6	22.2	3	1	LUXE_VIBFI	P24272 vibrio fisc
9	6	22.2	4	1	ACH1_ACHFU	P35904 achatina fu
10	6	22.2	4	1	DCML_PSECH	P19916 pseudomonas
11	6	22.2	4	1	EOSI_HUMAN	P02731 homo sapien
12	6	22.2	4	1	FAR3_HIRME	P42562 hirudo medi
13	6	22.2	4	1	FAR4_HIRME	P42563 hirudo medi
14	6	22.2	5	1	AL14_CARMA	P81817 carcinus ma
15	6	22.2	5	1	BIOA_CITFR	P13071 citrobacter
16	6	22.2	5	1	BIOA_SALTY	P12677 salmonella
17	6	22.2	5	1	FARP_ARTTR	P41853 artioposthi
18	6	22.2	5	1	SUGA_ACHDO	P19991 acheta dome
19	6	22.2	5	1	UC22_MAIZE	P80628 zea mays (m
20	6	22.2	5	1	UF01_MOUSE	P38639 mus musculu
21	5	18.5	4	1	TUFT_HUMAN	P01858 homo sapien
22	5	18.5	5	1	BIOB_SALTY	P12678 salmonella
23	5	18.5	5	1	PRCT_PERAM	P01373 periplaneta
24	4	14.8	4	1	RM01_YEAST	P36515 saccharomyc
25	2	7.4	4	1	DCMS_PSECH	P19918 pseudomonas
26	2	7.4	5	1	BPP7_BOTIN	P30425 bothrops in
27	1	3.7	3	1	THYL_PIG	P01151 sus scrofa
28	1	3.7	5	1	BIOB_CITFR	P12997 citrobacter

ALIGNMENTS

RESULT 1
UXA4_CHLTR
ID UXA4_CHLTR STANDARD; PRT; 5 AA.
AC P38005;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE UNKNOWN PROTEIN FROM 2D-PAGE FROM ELEMENTARY BODY (FRAGMENT).
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
RN [1]
RP SEQUENCE.
RC STRAIN=L2/434/BU;
RA Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,
RA Comanducci M., Christianen G., Birkelund S., Vtretou E., Ratti G.,
RA Pallini V.;
RL Submitted (SEP-1994) to the SWISS-PROT data bank.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.5, ITS MW IS: 28 KDA.
FT NON_TER 5 5
SQ SEQUENCE 5 AA; 474 MW; 75BAA865AA800000 CRC64;

Query Match 44.4%; Score 12; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GD 3
||
Db 3 GD 4

RESULT 2
TPIS_CANFA
ID TPIS_CANFA STANDARD; PRT; 5 AA.
AC P54714;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE TRIOSEPHOSPHATE ISOMERASE (EC 5.3.1.1) (TIM) (FRAGMENT).
GN TPI1.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
RN [1]
RP SEQUENCE.
RC TISSUE=HEART;
RX MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT dog heart proteins.";
RL Electrophoresis 18:2795-2802(1997).
CC -!- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE = DIHYDROXY-
CC ACETONE PHOSPHATE.
CC -!- PATHWAY: PLAYS AN IMPORTANT ROLE IN SEVERAL METABOLIC PATHWAYS.
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.
DR HSC-2DPAGE; P54714; DOG.
DR INTERPRO; IPR000652; -.
DR PROSITE; PS00171; TIM; PARTIAL.
KW Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
KW Pentose shunt.
FT NON_TER 1 1
FT NON_TER 5 5
SQ SEQUENCE 5 AA; 550 MW; 64444862C9A00000 CRC64;

Query Match 37.0%; Score 10; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FV 5
||

```
Db      1 FV 2


RESULT   3
PAP2_PARMA
ID   PAP2_PARMA     STANDARD;      PRT;     5 AA.
AC   P81864;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   01-OCT-2000 (Rel. 40, Last annotation update)
DE   PARDAXIN II (PXII) (FRAGMENT).
OS   Pardachirus marmoratus (Red sea moses sole).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC   Soleoidei; Soleidae; Pardachirus.
RN   [1]
RP   SEQUENCE.
RC   TISSUE=SKIN SECRETION;
RX   MEDLINE=87057369; PubMed=3782138;
RA   Lazarovici P., Primor N., Loew L.M.;
RT   "Purification and pore-forming activity of two hydrophobic
RT   polypeptides from the secretion of the Red sea moses sole (Pardachirus
RT   marmoratus).";
RL   J. Biol. Chem. 261:16704-16713(1986).
CC   -!- FUNCTION: EXHIBITS UNUSUAL SHARK REPELLENT AND SURFACTANT
CC       PROPERTIES. FORMS VOLTAGE-DEPENDENT, ION-PERMEABLE CHANNELS
CC       IN MEMBRANES. AT HIGH CONCENTRATION CAUSES CELL MEMBRANE LYSIS.
CC   -!- SUBUNIT: MONOMER. IN AQUEOUS SOLUTION EXISTS AS A TETRAMER.
CC   -!- SUBCELLULAR LOCATION: SECRETED.
CC   -!- SIMILARITY: BELONGS TO THE PARDAXIN FAMILY.
KW   Toxin.
FT   NON_TER       5      5
SQ   SEQUENCE   5 AA;  614 MW;  7769C9C9C8100000 CRC64;


  Query Match             33.3%;  Score 9;  DB 1;  Length 5;
  Best Local Similarity   66.7%;  Pred. No. 8.9e+04;
  Matches    2;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 GDF 4
          | |
Db      1 GFF 3


RESULT   4
TRM3_ECOLI
ID   TRM3_ECOLI     STANDARD;      PRT;     5 AA.
AC   P13973;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   TRAM PROTEIN (FRAGMENT).
GN   TRAM.
OS   Escherichia coli.
OG   Plasmid IncFII R100.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Escherichia.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88227859; PubMed=2836369;
RA   Inamoto S., Yoshioka Y., Ohtsubo E.;
RT   "Identification and characterization of the products from the traJ
RT   and traY genes of plasmid R100.";
RL   J. Bacteriol. 170:2749-2757(1988).
CC   -!- FUNCTION: TRANSFER GENE PROTEIN. IS INVOLVED IN THE CONJUGATION
CC       PROCESS OF BACTERIAL CELLS FOR THE EXCHANGE OF PLASMID DNA.
CC   -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC   -!- SIMILARITY: TO TRAM PROTEIN OF OTHER PLASMIDS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M20941; -; NOT_ANNOTATED_CDS.
DR   PIR; A32014; A32014.
KW   Conjugation; Plasmid; DNA-binding.
FT   NON_TER       1      1
SQ   SEQUENCE   5 AA;  634 MW;  6B1B1AA443500000 CRC64;


  Query Match             29.6%;  Score 8;  DB 1;  Length 5;
  Best Local Similarity   33.3%;  Pred. No. 8.9e+04;
  Matches    1;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 RGD 3
            : |
Db      1 KND 3


RESULT   5
FLRF_HIRME
ID   FLRF_HIRME     STANDARD;      PRT;     4 AA.
AC   P42561;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   01-NOV-1995 (Rel. 32, Last annotation update)
DE   FLRFAMIDE.
OS   Hirudo medicinalis (Medicinal leech), and Helisoma trivolvis (Snail).
OC   Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC   Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
RN   [1]
RP   SEQUENCE.
RC   SPECIES=H.MEDICINALIS;
RX   MEDLINE=92195954; PubMed=1686933;
RA   Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT   "Identification of RFamide neuropeptides in the medicinal leech.";
RL   Peptides 12:897-908(1991).
RN   [2]
RP   SEQUENCE.
RC   SPECIES=H.TRIVOLVIS; TISSUE=KIDNEY;
RX   MEDLINE=94286417; PubMed=7912428;
RA   Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT   "FMRFamide-related peptides from the kidney of the snail, Helisoma
RT   trivolvis.";
RL   Peptides 15:31-36(1994).
CC   -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC       FAMILY.
KW   Neuropeptide; Amidation.
FT   MOD_RES       4      4       AMIDATION.
SQ   SEQUENCE   4 AA;  582 MW;  69D40729A0000000 CRC64;


  Query Match             25.9%;  Score 7;  DB 1;  Length 4;
  Best Local Similarity   50.0%;  Pred. No. 8.9e+04;
  Matches    1;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 FV 5
            |:
Db      1 FL 2


RESULT   6
FMRF_MACNI
ID   FMRF_MACNI     STANDARD;      PRT;     4 AA.
AC   P01162;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   FMRFAMIDE (PEAK C) (CARDIOEXCITATORY NEUROPEPTIDE).
OS   Macrocallista nimbosa (Sun-ray clam), Nereis virens (Sandworm),
OS   Hirudo medicinalis (Medicinal leech), and Helisoma trivolvis (Snail).
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OC   Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroida;
OC   Veneroidea; Veneridae; Macrocallista.
RN   [1]
RP   SEQUENCE, AND SYNTHESIS.
RC   SPECIES=M.NIMBOSA; TISSUE=CEREBRAL PEDAL, AND VISCERAL GANGLION;
RX   MEDLINE=77215956; PubMed=877582;
RA   Price D.A., Greenberg M.J.;
RT   "Structure of a molluscan cardioexcitatory neuropeptide.";
RL   Science 197:670-671(1977).
RN   [2]
RP   SEQUENCE, AND CHARACTERIZATION.
RC   SPECIES=M.NIMBOSA; TISSUE=GANGLION;
RX   MEDLINE=78012038; PubMed=909875;
RA   Price D.A., Greenberg M.J.;
RT   "Purification and characterization of a cardioexcitatory neuropeptide
RT   from the central ganglia of a bivalve mollusc.";
RL   Prep. Biochem. 7:261-281(1977).
RN   [3]
RP   SEQUENCE.
RC   SPECIES=N.VIRENS;
RX   MEDLINE=90259866; PubMed=2342992;
RA   Krajniak K.G., Price D.A.;
RT   "Authentic FMRFamide is present in the polychaete Nereis virens.";
RL   Peptides 11:75-77(1990).
RN   [4]
RP   SEQUENCE.
RC   SPECIES=H.MEDICINALIS;
RX   MEDLINE=92195954; PubMed=1686933;
RA   Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT   "Identification of RFamide neuropeptides in the medicinal leech.";
RL   Peptides 12:897-908(1991).
RN   [5]
RP   SEQUENCE.
RC   SPECIES=H.TRIVOLVIS; TISSUE=KIDNEY;
RX   MEDLINE=94286417; PubMed=7912428;
RA   Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT   "FMRFamide-related peptides from the kidney of the snail, Helisoma
RT   trivolvis.";
RL   Peptides 15:31-36(1994).
CC   -!- FUNCTION: MYOACTIVE; CARDIOEXCITATORY SUBSTANCE. PHARMACOLOGICAL
CC       ACTIVITIES INCLUDE AUGMENTATION, INDUCTION, AND REGULARIZATION OF
CC       CARDIAC CONTRACTION.
CC   -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC       FAMILY.
DR   PIR; A01426; ECNK.
DR   PIR; A60418; A60418.
KW   Neuropeptide; Amidation.
FT   MOD_RES       4       4       AMIDATION.
SQ   SEQUENCE   4 AA;  600 MW;  69D40699A0000000 CRC64;


  Query Match             25.9%;  Score 7;  DB 1;  Length 4;
  Best Local Similarity   50.0%;  Pred. No. 8.9e+04;
  Matches    1;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 FV 5
          |:
Db      1 FM 2


RESULT   7
GRWM_HUMAN
ID   GRWM_HUMAN     STANDARD;      PRT;     3 AA.
AC   P01157;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   21-JUL-1986 (Rel. 01, Last annotation update)
DE   GROWTH-MODULATING PEPTIDE.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=77162369; PubMed=858356;
RA   Schlesinger D.H., Pickart L., Thaler M.M.;
RT   "Growth-modulating serum tripeptide is glycyl-histidyl-lysine.";
RL   Experientia 33:324-325(1977).
CC   -!- MISCELLANEOUS: THIS SERUM TRIPEPTIDE HAS BEEN FOUND TO STIMULATE
CC       GROWTH OF SOME CELL TYPES AND TO INHIBIT OTHER TYPES IN VITRO.
DR   PIR; A01421; GKHU.
SQ   SEQUENCE   3 AA;  340 MW;  6331E81000000000 CRC64;


  Query Match             22.2%;  Score 6;  DB 1;  Length 3;
  Best Local Similarity   100.0%;  Pred. No. 8.9e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 G 2
          |
Db      1 G 1


RESULT   8
LUXE_VIBFI
ID   LUXE_VIBFI     STANDARD;      PRT;     3 AA.
AC   P24272;
DT   01-MAR-1992 (Rel. 21, Created)
DT   01-MAR-1992 (Rel. 21, Last sequence update)
DT   01-OCT-1996 (Rel. 34, Last annotation update)
DE   LONG-CHAIN-FATTY-ACID--LUCIFERIN-COMPONENT LIGASE (EC 6.2.1.19)
DE   (ACYL-PROTEIN SYNTHETASE) (FRAGMENT).
GN   LUXE.
OS   Vibrio fischeri.
OC   Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91072225; PubMed=2254256;
RA   Swartzman E., Kapoor S., Graham A.F., Meighen E.A.;
RT   "A new Vibrio fischeri lux gene precedes a bidirectional termination
RT   site for the lux operon.";
RL   J. Bacteriol. 172:6797-6802(1990).
CC   -!- FUNCTION: ACYL-PROTEIN SYNTHETASE ACTIVATES TETRADECANOIC ACID.
CC       IT IS A COMPONENT OF THE FATTY ACID REDUCTASE COMPLEX RESPONSIBLE
CC       FOR CONVERTING TETRADECANOIC ACID TO THE ALDEHYDE WHICH SERVES AS
CC       SUBSTRATE IN THE LUCIFERASE-CATALYZED REACTION.
CC   -!- CATALYTIC ACTIVITY: ATP + AN ACID + PROTEIN = AMP + PYROPHOSPHATE
CC       + AN ACYL-PROTEIN THIOLESTER.
CC   -!- PATHWAY: SECOND STEP IN THE BIOLUMINESCENT FATTY ACID REDUCTASE
CC       COMPLEX.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   ----------------------------------------------------------------------
DR   EMBL; M62812; -; NOT_ANNOTATED_CDS.
KW   Luminescence; Ligase.
FT   NON_TER       1       1
SQ   SEQUENCE   3 AA;  374 MW;  6AA3303000000000 CRC64;


  Query Match             22.2%;  Score 6;  DB 1;  Length 3;
  Best Local Similarity   100.0%;  Pred. No. 8.9e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 D 3
          |
Db      3 D 3


RESULT   9
ACH1_ACHFU
ID   ACH1_ACHFU     STANDARD;      PRT;     4 AA.
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AC   P35904;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   ACHATIN-I.
OS   Achatina fulica (Giant African snail).
OC   Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC   Achatinacea; Achatinidae; Achatina.
RN   [1]
RP   SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.
RC   STRAIN=FERUSSAC; TISSUE=GANGLION;
RX   MEDLINE=89273551; PubMed=2597281;
RA   Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,
RA   Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Li P.,
RA   Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.;
RT   "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina
RT   fulica Ferussac containing a D-amino acid residue.";
RL   Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
RN   [2]
RP   CHARACTERIZATION.
RC   STRAIN=FERUSSAC; TISSUE=HEART ATRIUM;
RX   MEDLINE=91264856; PubMed=1675568;
RA   Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,
RA   Yoshida M., Harada A., Muneoka Y., Kobayashi M.;
RT   "Purification of achatin-I from the atria of the African giant snail,
RT   Achatina fulica, and its possible function.";
RL   Biochem. Biophys. Res. Commun. 177:847-853(1991).
RN   [3]
RP   X-RAY CRYSTALLOGRAPHY.
RX   MEDLINE=93014529; PubMed=1399265;
RA   Ishida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,
RA   Iwashita T., Nomoto K.;
RT   "Crystal structure and molecular conformation of achatin-I
RT   (H-Gly-D-Phe-Ala-Asp-OH), an endogenous neuropeptide containing a
RT   D-amino acid residue.";
RL   Int. J. Pept. Protein Res. 39:258-264(1992).
CC   -!- FUNCTION: NEUROEXCITATORY PEPTIDE; INCREASES THE IMPULSE FREQUENCY
CC       AND PRODUCES A SPIKE BROADENING OF THE IDENTIFIED HEART EXCITATORY
CC       NEURON (PON); ALSO ENHANCES THE AMPLITUDE AND FREQUENCY OF THE
CC       HEART BEAT. HAS ALSO AN EFFECT ON SEVERAL OTHER MUSCLES.
DR   PIR; A32480; A32480.
KW   Hormone; D-amino acid.
FT   MOD_RES       2       2       D-PHENYLALANINE.
SQ   SEQUENCE   4 AA;  408 MW;  6AADD9C810000000 CRC64;


  Query Match             22.2%;  Score 6;  DB 1;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 8.9e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 G 2
          |
Db      1 G 1


RESULT  10
DCML_PSECH
ID   DCML_PSECH     STANDARD;      PRT:     4 AA.
AC   P19916;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   01-DEC-1992 (Rel. 24, Last annotation update)
DE   CARBON MONOXIDE DEHYDROGENASE LARGE CHAIN (EC 1.2.99.2) (FRAGMENT).
OS   Pseudomonas carboxydohydrogena.
OC   Bacteria; Proteobacteria.
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=90055678; PubMed=2818128;
RA   Kraut M., Hugendieck I., Herwig S., Meyer O.;
RT   "Homology and distribution of CO dehydrogenase structural genes in
RT   carboxydotrophic bacteria.";
RL   Arch. Microbiol. 152:335-341(1989).
CC   -!- CATALYTIC ACTIVITY: CO + H(2)O + ACCEPTOR = CO(2) + REDUCED
CC       ACCEPTOR.
CC   -!- COFACTOR: MOLYBDENUM.
CC   -!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
CC       SMALL.
DR   PIR; PL0140; PL0140.
KW   Oxidoreductase; Molybdenum.
FT   NON_TER       4       4
SQ   SEQUENCE   4 AA;  441 MW;  7761E876F0000000 CRC64;


  Query Match             22.2%;  Score 6;  DB 1;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 8.9e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 G 2
          |
Db      2 G 2


RESULT  11
EOSI_HUMAN
ID   EOSI_HUMAN     STANDARD;      PRT:     4 AA.
AC   P02731;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   21-JUL-1986 (Rel. 01, Last annotation update)
DE   EOSINOPHILOTACTIC PEPTIDES.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=76078412; PubMed=1060093;
RA   Goetzl E.J., Austen K.F.;
RT   "Purification and synthesis of eosinophilotactic tetrapeptides of
RT   human lung tissue: identification as eosinophil chemotactic factor of
RT   anaphylaxis.";
RL   Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).
CC   -!- MISCELLANEOUS: THESE PEPTIDES ARE RELEASED FROM MAST CELLS IN LUNG
CC       (AND OTHER TISSUES) DURING HYPERSENSITIVITY REACTIONS
CC       (ANAPHYLAXIS). THEIR ACTIVITIES, PREFERENTIALLY AFFECTING
CC       EOSINOPHILS, INCLUDE CHEMOTAXIS, CHEMOTACTIC DEACTIVATION, RELEASE
CC       OF ENZYMES, AND STIMULATION OF THE HEXOSE MONOPHOSPHATE SHUNT.
DR   PIR; A03190; ETHUL.
FT   VARIANT       1       1       V -> A (IN OTHER PEPTIDE).
FT                                 /FTId=VAR_005201.
SQ   SEQUENCE   4 AA;  390 MW;  6B05B862A0000000 CRC64;


  Query Match             22.2%;  Score 6;  DB 1;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 8.9e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 G 2
          |
Db      2 G 2


RESULT  12
FAR3_HIRME
ID   FAR3_HIRME     STANDARD;      PRT:     4 AA.
AC   P42562;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   01-NOV-1995 (Rel. 32, Last annotation update)
DE   FMRFAMIDE-LIKE NEUROPEPTIDE YLRF-AMIDE.
OS   Hirudo medicinalis (Medicinal leech).
OC   Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC   Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=92195954; PubMed=1686933;
RA   Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
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```
RT   "Identification of RFamide neuropeptides in the medicinal leech.";
RL   Peptides 12:897-908(1991).
CC   -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC       FAMILY.
KW   Neuropeptide; Amidation.
FT   MOD_RES       4       4       AMIDATION.
SQ   SEQUENCE   4 AA;  598 MW;  69D4073B30000000 CRC64;


  Query Match             22.2%;  Score 6;  DB 1;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 8.9e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 F 4
          |
Db      4 F 4


RESULT  13
FAR4_HIRME
ID   FAR4_HIRME     STANDARD;      PRT;     4 AA.
AC   P42563;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   01-NOV-1995 (Rel. 32, Last annotation update)
DE   FMRFAMIDE-LIKE NEUROPEPTIDE YMRF-AMIDE.
OS   Hirudo medicinalis (Medicinal leech).
OC   Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC   Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=92195954; PubMed=1686933;
RA   Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT   "Identification of RFamide neuropeptides in the medicinal leech.";
RL   Peptides 12:897-908(1991).
CC   -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC       FAMILY.
KW   Neuropeptide; Amidation.
FT   MOD_RES       4       4       AMIDATION.
SQ   SEQUENCE   4 AA;  616 MW;  69D4068B30000000 CRC64;


  Query Match             22.2%;  Score 6;  DB 1;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 8.9e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 F 4
          |
Db      4 F 4


RESULT  14
AL14_CARMA
ID   AL14_CARMA     STANDARD;      PRT;     5 AA.
AC   P81817;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   CARCINUSTATIN 14.
OS   Carcinus maenas (Common shore crab) (Green crab).
OC   Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC   Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC   Eubrachyura; Portunoidea; Portunidae; Carcinus.
RN   [1]
RP   SEQUENCE.
RC   TISSUE=CEREBRAL GANGLION, AND THORACIC GANGLION;
RX   MEDLINE=98121193; PubMed=9461295;
RA   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA   Thorpe A.;
RT   "Isolation and identification of multiple neuropeptides of the
RT   allatostatin superfamily in the shore crab Carcinus maenas.";
RL   Eur. J. Biochem. 250:727-734(1997).
CC   -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC   -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW   Neuropeptide; Amidation; Multigene family.
FT   MOD_RES       5       5       AMIDATION (POTENTIAL).
SQ   SEQUENCE   5 AA;  586 MW;  672879D5AB300000 CRC64;


  Query Match             22.2%;  Score 6;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 8.9e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 F 4
          |
Db      3 F 3


RESULT  15
BIOA_CITFR
ID   BIOA_CITFR     STANDARD;      PRT;     5 AA.
AC   P13071;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   01-DEC-1992 (Rel. 24, Last annotation update)
DE   ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE
DE   (EC 2.6.1.62) (7,8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA
DE   AMINOTRANSFERASE) (FRAGMENT).
GN   BIOA.
OS   Citrobacter freundii.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Citrobacter.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89006280; PubMed=2971595;
RA   Shiuan D., Campbell A.;
RT   "Transcriptional regulation and gene arrangement of Escherichia coli,
RT   Citrobacter freundii and Salmonella typhimurium biotin operons.";
RL   Gene 67:203-211(1988).
CC   -!- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + 8-AMINO-7-
CC       OXONONANOATE = S-ADENOSYL-4-METHYLTHIO-2-OXOBUTANOATE +
CC       7,8-DIAMINONONANOATE.
CC   -!- COFACTOR: PYRIDOXAL PHOSPHATE.
CC   -!- PATHWAY: BIOTIN BIOSYNTHESIS.
CC   -!- SUBUNIT: HOMODIMER.
CC   -!- SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC       AMINOTRANSFERASES.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M21922; CAB25179.1; -.
DR   INTERPRO; IPR000954; -.
DR   PROSITE; PS00600; AA_TRANSFER_CLASS_3; PARTIAL.
KW   Biotin biosynthesis; Transferase; Aminotransferase;
KW   Pyridoxal phosphate.
FT   NON_TER       5       5
SQ   SEQUENCE   5 AA;  582 MW;  6AAAB1B1A6F00000 CRC64;


  Query Match             22.2%;  Score 6;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 8.9e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 D 3
          |
Db      4 D 4


Search completed: March  6, 2001, 09:48:22
```

Job time: 180 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: March 6, 2001, 09:48:05 ; Search time 32.72 Seconds
(without alignments)
17.911 Million cell updates/sec

Title: US-09-081-522-7
Perfect score: 27
Sequence: 1 RGDFV 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 8

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_15:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	12	44.4	5	13	P82070	P82070 litoria rub
2	10	37.0	5	13	P82099	P82099 litoria rub
3	9	33.3	5	13	P82073	P82073 litoria rub
4	9	33.3	5	13	P82100	P82100 litoria rub
5	8	29.6	5	13	P82071	P82071 litoria rub
6	8	29.6	5	13	P82072	P82072 litoria rub
7	4	14.8	4	11	Q08433	Q08433 rattus norv
8	2	7.4	5	10	Q99007	Q99007 hordeum vul

ALIGNMENTS

RESULT 1
P82070
ID P82070 PRELIMINARY; PRT; 5 AA.
AC P82070;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE RUBELLIDIN 1.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=SKIN SECRETION;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australin red tree frog
RT 'Litoria rubella'. the skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
CC -!- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
CC ANTIBIOTIC ACTIVITY.
CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -!- MASS SPECTROMETRY: MW=598; METHOD=FAB.
KW Amphibian skin.
SQ SEQUENCE 5 AA; 598 MW; 6DD9C9CAB2A00000 CRC64;

Query Match 44.4%; Score 12; DB 13; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      3 DF 4
          ||
Db      2 DF 3
```

RESULT 2
P82099
ID P82099 PRELIMINARY; PRT; 5 AA.
AC P82099;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE ELECTRIN 3.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=SKIN SECRETION;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litori electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:0-0(1999).
KW Amphibian skin; Amidation.
FT MOD_RES 5 5 AMIDATION.
SQ SEQUENCE 5 AA; 630 MW; 658761F2C9A00000 CRC64;

Query Match 37.0%; Score 10; DB 13; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      4 FV 5
          ||
Db      1 FV 2
```

RESULT 3
P82073
ID P82073 PRELIMINARY; PRT; 5 AA.
AC P82073;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)

```
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   RUBELLIDIN 3.2.
OS   Litoria rubella (Desert tree frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC   Litoria.
OX   NCBI_TaxID=104895;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=SKIN SECRETION;
RA   Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT   "Peptides from the skin glands of the Australian buzzing tree frog
RT   Litori electrica. Comparison with the skin peptides from Litoria
RT   rubella.";
RL   Aust. J. Chem. 52:0-0(1999).
CC   -!- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
CC       ANTIBIOTIC ACTIVITY.
CC   -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
KW   Amphibian skin.
SQ   SEQUENCE   5 AA;  570 MW;  71A9C9C862A00000 CRC64;


  Query Match             33.3%;  Score 9;  DB 13;  Length 5;
  Best Local Similarity   66.7%;  Pred. No. 3.7e+05;
  Matches    2;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 GDF 4
           | |
Db       2 GFF 4


RESULT   4
P82100
ID   P82100      PRELIMINARY;      PRT;     5 AA.
AC   P82100;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   ELECTRIN 4.
OS   Litoria rubella (Desert tree frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC   Litoria.
OX   NCBI_TaxID=104895;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=SKIN SECRETION;
RA   Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT   "Peptides from the skin glands of the Australian buzzing tree frog
RT   Litori electrica. Comparison with the skin peptides from Litoria
RT   rubella.";
RL   Aust. J. Chem. 52:0-0(1999).
KW   Amphibian skin; Amidation.
FT   MOD_RES       5       5       AMIDATION.
SQ   SEQUENCE   5 AA;  616 MW;  61F2D1A059A00000 CRC64;


  Query Match             33.3%;  Score 9;  DB 13;  Length 5;
  Best Local Similarity   50.0%;  Pred. No. 3.7e+05;
  Matches    1;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 FV 5
           |:
Db       1 FI 2


RESULT   5
P82071
ID   P82071      PRELIMINARY;      PRT;     5 AA.
AC   P82071;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   RUBELLIDIN 2.1.
OS   Litoria rubella (Desert tree frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC   Litoria.
OX   NCBI_TaxID=104895;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=SKIN SECRETION;
RA   Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA   Tyler M.J., Wallace J.C.;
RT   "The structure of new peptides from the Australin red tree frog
RT   'Litoria rubella'. the skin peptide profile as a probe for the study
RT   of evolutionary trends of amphibians.";
RL   Aust. J. Chem. 49:955-963(1996).
CC   -!- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
CC       ANTIBIOTIC ACTIVITY.
CC   -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC   -!- MASS SPECTROMETRY: MW=626; METHOD=FAB.
KW   Amphibian skin.
SQ   SEQUENCE   5 AA;  625 MW;  6DD9C9CB10300000 CRC64;


  Query Match             29.6%;  Score 8;  DB 13;  Length 5;
  Best Local Similarity   50.0%;  Pred. No. 3.7e+05;
  Matches    1;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 DF 4
           :|
Db       2 EF 3


RESULT   6
P82072
ID   P82072      PRELIMINARY;      PRT;     5 AA.
AC   P82072;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   RUBELLIDIN 3.1.
OS   Litoria rubella (Desert tree frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC   Litoria.
OX   NCBI_TaxID=104895;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=SKIN SECRETION;
RA   Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA   Tyler M.J., Wallace J.C.;
RT   "The structure of new peptides from the Australin red tree frog
RT   'Litoria rubella'. the skin peptide profile as a probe for the study
RT   of evolutionary trends of amphibians.";
RL   Aust. J. Chem. 49:955-963(1996).
CC   -!- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
CC       ANTIBIOTIC ACTIVITY.
CC   -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC   -!- MASS SPECTROMETRY: MW=655; METHOD=FAB.
KW   Amphibian skin; Amidation.
FT   MOD_RES       5       5       AMIDATION.
SQ   SEQUENCE   5 AA;  656 MW;  71A9C9CB10300000 CRC64;


  Query Match             29.6%;  Score 8;  DB 13;  Length 5;
  Best Local Similarity   50.0%;  Pred. No. 3.7e+05;
  Matches    1;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 DF 4
           :|
Db       2 EF 3
```

```
RESULT   7
Q08433
ID   Q08433      PRELIMINARY;      PRT;     4 AA.
AC   Q08433;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
DE   UDP-GLUCURONOSYLTRANSFERASE, MICROSOMAL (EC 2.4.1.17) (UDPGT)
DE   (FRAGMENT).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=GUNN;
RX   MEDLINE=91282758; PubMed=1840486;
RA   Sato H., Aono S., Kashiwamata S., Koiwai O.;
RT   "Genetic defect of bilirubin UDP-glucuronosyltransferase in the
RT   hyperbilirubinemic Gunn rat.";
RL   Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
CC   -!- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
CC       SUBSEQUENT ELIMINATION OF PCTENTIALLY TOXIC XENOBIOTICS AND
CC       ENDOGENOUS COMPOUNDS.
CC   -!- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
CC       BETA-D-GLUCORONOSIDE.
CC   -!- SUBCELLULAR LOCATION: MICROSOME.
DR   EMBL; S38636; AAB19259.1; -.
KW   Transferase; Glycosyltransferase; Microsome; Multigene family.
FT   NON_TER       1      1
FT   NON_TER       4      4
SQ   SEQUENCE   4 AA;  473 MW;  633732C420000000 CRC64;


  Query Match             14.8%;  Score 4;  DB 11;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 V 5
           |
Db       2 V 2


RESULT   8
Q99007
ID   Q99007      PRELIMINARY;      PRT;     5 AA.
AC   Q99007;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   ALPHA-AMYLASE (EC 3.2.1.1) (FRAGMENT).
GN   AMY1.
OS   Hordeum vulgare (Barley).
OC   Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC   Magnoliophyta; Liliopsida; Poales; Poaceae; Hordeum.
OX   NCBI_TaxID=4513;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=HIMALAYA; TISSUE=ALEURONE LAYER;
RX   MEDLINE=91329704; PubMed=1831055;
RA   Jacobsen J.V., Close T.J.;
RT   "Control of transient expression of chimaeric genes by gibberellic
RT   acid and abscisic acid in protoplasts prepared from mature barley
RT   aleurone layers.";
RL   Plant Mol. Biol. 16:713-721(1991).
CC   -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC
CC       LINKAGES IN OLIGOSACCHARIDES AND POLYASACCHARIDES.
CC   -!- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC   -!- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN
CC       BARLEY.
DR   EMBL; X54643; CAA38455.1; -.
KW   Hydrolase; Glycosidase; Carbohydrate metabolism; Seed; Germination;
KW   Calcium; Multigene family.
FT   NON_TER       5      5
SQ   SEQUENCE   5 AA;  600 MW;  61E3344DD6F00000 CRC64;


  Query Match             7.4%;  Score 2;  DB 10;  Length 5;
  Best Local Similarity   0.0%;  Pred. No. 3.7e+05;
  Matches    0;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 R 1
           :
Db       4 K 4


Search completed: March  6, 2001, 09:48:05
Job time: 191 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: March 6, 2001, 09:45:58 ; Search time 14.72 Seconds
(without alignments)
34.844 Million cell updates/sec

Title: US-09-081-522-8
Perfect score: 83
Sequence: 1 YTAECKPQVTRGDVF 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 107883

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_36:*
1: /SIDS1/gcgdata/geneseq/geneseqp/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqp/AA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqp/AA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqp/AA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqp/AA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqp/AA1985.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseqp/AA1986.DAT:*
8: /SIDS1/gcgdata/geneseq/geneseqp/AA1987.DAT:*
9: /SIDS1/gcgdata/geneseq/geneseqp/AA1988.DAT:*
10: /SIDS1/gcgdata/geneseq/geneseqp/AA1989.DAT:*
11: /SIDS1/gcgdata/geneseq/geneseqp/AA1990.DAT:*
12: /SIDS1/gcgdata/geneseq/geneseqp/AA1991.DAT:*
13: /SIDS1/gcgdata/geneseq/geneseqp/AA1992.DAT:*
14: /SIDS1/gcgdata/geneseq/geneseqp/AA1993.DAT:*
15: /SIDS1/gcgdata/geneseq/geneseqp/AA1994.DAT:*
16: /SIDS1/gcgdata/geneseq/geneseqp/AA1995.DAT:*
17: /SIDS1/gcgdata/geneseq/geneseqp/AA1996.DAT:*
18: /SIDS1/gcgdata/geneseq/geneseqp/AA1997.DAT:*
19: /SIDS1/gcgdata/geneseq/geneseqp/AA1998.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseqp/AA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqp/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	83	100.0	15	16	R82390	Integrin alpha-v-b
2	83	100.0	15	18	W33058	Alpha-v, beta-5 vi
3	83	100.0	15	19	W41102	Alpha-v beta-3 ant
4	83	100.0	15	19	W41244	Alpha-v-beta-5 ant
5	48	57.8	15	16	R67663	Synthetic peptide
6	36	43.4	9	19	W66820	Peptide used in pu
7	36	43.4	9	20	W97014	Peptide used to in
8	30	36.1	10	19	W68121	Human bone apposit
9	30	36.1	10	19	W68122	Human bone apposit
10	30	36.1	10	19	W68119	Human bone apposit
11	29	34.9	11	13	R24067	Cell-to-cell bindi
12	28	33.7	11	11	R06020	Oligopeptide, anti
13	28	33.7	12	16	R76241	Human Fas peptide
14	28	33.7	12	21	Y84806	Internal peptide o
15	28	33.7	13	17	R95959	Heterologous prote
16	27.5	33.1	11	21	Y81884	Yeast SAH1 protein
17	27	32.5	8	15	R50462	Antiproliferative
18	27	32.5	10	18	W22349	Human bone apposit
19	27	32.5	10	19	W68120	Human bone apposit
20	27	32.5	10	19	W68123	Human bone apposit
21	27	32.5	10	19	W68129	Human bone apposit
22	27	32.5	10	19	W68130	Human bone apposit
23	27	32.5	10	19	W68109	Human bone apposit
24	27	32.5	10	19	W68117	Human bone apposit
25	27	32.5	10	19	W68124	Human bone apposit
26	27	32.5	10	19	W68125	Human bone apposit
27	27	32.5	10	19	W68128	Human bone apposit
28	27	32.5	11	18	W22356	Human bone apposit
29	27	32.5	11	19	W68116	Human bone apposit
30	27	32.5	14	18	W22348	Human bone apposit
31	27	32.5	14	19	W68108	Human bone apposit
32	27	32.5	15	18	W22347	Human bone apposit
33	27	32.5	15	19	W68107	Human bone apposit
34	26	31.3	9	13	R21425	Matrix peptide fro
35	26	31.3	9	20	W97047	Peptide used to in
36	26	31.3	9	20	W96982	Peptide used to in
37	26	31.3	10	19	W54456	Human native angio
38	26	31.3	10	21	Y70262	Peptide encoded by
39	26	31.3	12	18	W23803	VEGF/VPF antigen s
40	26	31.3	12	19	W74628	Amino acid sequenc
41	26	31.3	12	19	W74689	Amino acid sequenc
42	26	31.3	12	19	W74690	Amino acid sequenc
43	26	31.3	12	19	W55952	Human vascular per
44	26	31.3	12	19	W55953	Human vascular per
45	26	31.3	12	19	W55951	Human vascular per

ALIGNMENTS

RESULT 1
R82390
ID R82390 standard; peptide; 15 AA.
XX
AC R82390;
XX
DT 03-MAY-1996 (first entry)
XX
DE Integrin alpha-v-beta-3 inhibitor peptide no. 62880.
XX
KW Integrin; alpha-v-beta-3; inhibitor; angiogenesis; antagonist;
KW fibrinogen; inflammation; apoptosis; restenosis.
XX
OS Synthetic.
XX
PN WO9525543-A1.
XX
PD 28-SEP-1995.
XX
PF 09-MAR-1995; 95WO-US03035.
XX
PR 30-DEC-1994; 94US-0366665.
PR 18-MAR-1994; 94US-0210715.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Brooks P, Cheresh DA;
XX
DR WPI; 1995-344463/44.
XX
PT Inhibition of angiogenesis in a tissue, e.g. following angioplasty
PT - by admin. of a compsn. comprising an alpha-v-beta3 antagonist,
PT useful for regression of established tumours, treating inflamed
PT tissue, etc.
XX

PS Claim 4; Page 47; 135pp; English.
XX
CC R82386-96 are a group of inhibitor peptides of integrin alpha-v-beta-3.
CC The inhibitor peptides may be administered in a compsn. and are useful
CC for inhibition of inflamed tissue angiogenesis, e.g. that associated
CC with rheumatoid arthritis, retinal angiogenesis associated with
CC diabetic retinopathy, that associated with haemangioma, solid
CC tumours, or solid tumour metastases. The alpha-v-beta-3 atagonists
CC are also useful to induce apoptosis in neovasculature in a tissue.
CC The inhibitor peptides are pref. cyclic and contain an RGD sequence.
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 83; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.5e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTAECKPQVTRGDVF 15
||||||||||||||||
Db 1 ytaeckpqvtrgdvf 15

RESULT 2
W33058
ID W33058 standard; peptide; 15 AA.
XX
AC W33058;
XX
DT 26-JAN-1998 (first entry)
XX
DE Alpha-v, beta-5 vitronectin receptor antagonist.
XX
KW RGD containing peptide; antagonist; alpha-v, beta-5;
KW vitronectin receptor; inhibition; angiogenesis; inflammation;
KW rheumatoid arthritis; eye disease; diabetic retinopathy;
KW age related macular degeneration; ocular histoplasmosis;
KW retinopathy; prematurity; neovascular glaucoma;
KW corneal neovascular disorder; transplantation; herpetic; luetic;
KW keratitis; pterygium; neovascular pannus; haemangioma;
KW solid tumour; metastasis; cytokine; low toxicity;
KW vascular endothelial growth factor;
KW transforming growth factor alpha; epidermal growth factor.
XX
OS Synthetic.
XX
PN WO9706791-A1.
XX
PD 27-FEB-1997.
XX
PF 13-AUG-1996; 96WO-US13194.
XX
PR 14-AUG-1995; 95US-0514799.
PR 14-AUG-1996; 96ZA-0006886.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Brooks P, Cheresh DA, Friedlander M;
XX
DR WPI; 1997-165019/15.
XX
PT Inhibiting angiogenesis with an antagonist selective for the
PT alpha-v,beta-5 integrin receptor - e.g. antibody, RGD peptide or
PT organic mimetic, for treatment of inflammation, eye disease, tumours
PT etc.
XX
PS Claim 5; Page 105; 126pp; English.
XX
CC The present RGD containing peptide is an antagonist of the alpha-v,
CC beta-5 vitronectin receptor, which can be used to inhibit
CC angiogenesis in alpha-v, beta-5 containing tissue, specifically
CC angiogenesis as a result of inflammation (especially rheumatoid
CC arthritis), eye disease (especially diabetic retinopathy, age
CC related macular degeneration, ocular histoplasmosis, retinopathy of
CC prematurity or neovascular glaucoma), corneal neovascular disorders
CC (especially transplantation, herpetic or luetic keratitis,
CC pterygium and neovascular pannus associated with wearing contact
CC lenses), haemangioma, solid tumours and their metastases or
CC cytokines (especially vascular endothelial growth factor,
CC transforming growth factor alpha or epidermal growth factor). The
CC antagonist has the advantage of being very specific, affecting no
CC processes other than angiogenesis and therefore of relatively low
CC toxicity.
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 83; DB 18; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.5e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTAECKPQVTRGDVF 15
||||||||||||||||
Db 1 ytaeckpqvtrgdvf 15

RESULT 3
W41102
ID W41102 standard; Peptide; 15 AA.
XX
AC W41102;
XX
DT 08-JUN-1998 (first entry)
XX
DE Alpha-v beta-3 antagonist linear peptide 62880.
XX
KW Angiogenesis; inhibitor; antagonist; integrin alpha-v beta-3;
KW vitronectin receptor; rheumatoid arthritis; tumour; metastasis;
KW diabetic retinopathy; macular degeneration; restenosis; therapy.
XX
OS Synthetic.
XX
PN WO9745137-A1.
XX
PD 04-DEC-1997.
XX
PF 30-MAY-1997; 97WO-US09158.
XX
PR 31-MAY-1996; 96US-0018733.
PR 31-MAY-1996; 96US-0015869.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Brooks P, Cheresh DA;
XX
DR WPI; 1998-032334/03.
XX
PT Packaging material containing polypeptide antagonist of alphav,
PT beta3 integrin - used for inhibition of angiogenesis, and for
PT treating tumours, inflammation, eye diseases etc.
XX
PS Example 1; Page 51; 234pp; English.
XX
CC This RGD-containing linear peptide, designated 62880, corresponds
CC to amino acid residues of 35-49 of vitronectin. It is a
CC particularly preferred peptide that has integrin alpha-v beta-3
CC antagonist activity. It exhibits preferential inhibition of
CC fibrinogen or vitronectin binding to the alpha-v beta-3 receptor.
CC Peptide 62880 can be prepared using standard solid-phase synthesis
CC techniques. The invention relates to the discovery that
CC angiogenesis is mediated by the specific vitronectin receptor
CC alpha-v beta-3, and that inhibition of alpha-v beta-3 function
CC inhibits angiogenesis. Claimed antagonists of alpha-v beta-3
CC comprise C-terminal fragments (see W41083-94) of human or chicken
CC matrix metalloproteinase-2, fusion polypeptides, cyclic or linear
CC polypeptides, derivatised polypeptides, a monoclonal antibody or

CC organic mimetic compound. They can be used to inhibit angiogenesis
CC in inflammed tissue (for treatment of arthritis or rheumatoid
CC arthritis), in solid tumours or metastases (particularly to induce
CC regression or inhibit tumour growth), and in ocular disorders such
CC as diabetic retinopathy and macular degeneration, as well as to
CC treat restenosis (all claimed).
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 83; DB 19; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.5e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTAECKPQVTRGDVF 15
||||||||||||||||
Db 1 ytaeckpqvtrgdvf 15

RESULT 4
W41244
ID W41244 standard; protein; 15 AA.
XX
AC W41244;
XX
DT 09-JUN-1998 (first entry)
XX
DE Alpha-v-beta-5 antagonistic peptide 62880.
XX
KW Alpha-v-beta-5 antagonist; treatment; vitronectin receptor; inhibition;
KW angiogenesis; tumour growth; restenosis; neovascularisation.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1..15
FT /note= "peptide is made cyclic via the first and
FT last residues"
XX
PN WO9745447-A1.
XX
PD 04-DEC-1997.
XX
PF 30-MAY-1997; 97WO-US09099.
XX
PR 31-MAY-1996; 96US-0018733.
PR 31-MAY-1996; 96US-0015869.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Brooks P, Cheresh DA, Friedlander M;
XX
DR WPI; 1998-041758/04.
XX
PT Packaging material containing polypeptide antagonist of alphav,
PT beta5 integrin - used for inhibition of angiogenesis, and for
PT treating tumours, inflammation, eye diseases etc.
XX
PS Disclosure; Page 41; 117pp; English.
XX
CC The present peptide represents an alpha-v-beta-5 integrin antagonists.
CC Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of alpha-v-beta-5
CC can inhibit angiogenesis. The specification describes a novel
CC labelled package that contains an inhibitor of angiogenesis i.e. an
CC alpha-v-beta-5 antagonising polypeptide that binds to integrin
CC alpha-v-beta-5 and includes a part of the C-terminal domain of MMP-2.
CC The antagonists are used to inhibit angiogenesis in inflamed tissue, in
CC solid tumours or metastases, and in a wide range of ocular disorders
CC (e.g. diabetic or other forms of retinopathy, neovascular glaucoma, or
CC corneal transplants). They are particularly used to induce regression or
CC to inhibit growth of tumours. The alpha-v-beta-5 antagonists can also be
CC used to treat restenosis caused by migration of smooth muscle cells
CC following angioplasty and to reduce blood supply to selected tissues.
CC The antagonists particularly inhibit neovascularisation where this is
CC induced by cytokines, e.g. transforming growth factor alpha, epidermal
CC growth factor or especially vascular endothelial growth factor.
CC note: this sequence does not appear in the specification; it was created
CC using information provided.
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 83; DB 19; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.5e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTAECKPQVTRGDVF 15
||||||||||||||||
Db 1 ytaeckpqvtrgdvf 15

RESULT 5
R67663
ID R67663 standard; peptide; 15 AA.
XX
AC R67663;
XX
DT 07-AUG-1995 (first entry)
XX
DE Synthetic peptide of cell-adhesive molecule vitronectin.
XX
KW Influenza; nucleoprotein; immunoglobulin; NP; CDR: Ig;
KW complementarity determining region; epitope; antigen; tolerance;
KW hypersensitivity; immunity; pathogen.
XX
OS Synthetic.
XX
PN WO9428026-A.
XX
PD 08-DEC-1994.
XX
PF 25-MAY-1994; 94WO-US06090.
XX
PR 28-MAY-1993; 93US-0068895.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Billetta R, Zanetti M;
XX
DR WPI; 1995-022720/03.
XX
PT New immunoglobulin contg. influenza virus nucleoprotein epitope
PT - useful in vaccines to induce specific anti-viral immunity, also
PT related DNA, vectors and transfected host cells
XX
PS Example 1B; Page 23; 62pp; English.
XX
CC Influenza virus nucleoprotein (NP) epitopes may be inserted into
CC immunoglobulin complementarity determining regions to render the
CC immunoglobulin molecule antigenic, making it useful as a vaccine.
CC Such antigenised antibodies can be used can be used to induce
CC tolerance to particular antigens (including those associated with
CC autoimmune diseases); to down-regulate hypersensitivity to allergens,
CC or to provide active or passive immunity against pathogenic antigens.
CC The antigenic immunoglobulins are fully functional as regards
CC localisation on cell or receptor sites and elicit cytotoxic T
CC lymphocytes specific for the incorporated epitope. This synthetic
CC peptide corresponds to a region of the cell-adhesive molecule
CC vitronectin.
XX
SQ Sequence 15 AA;

Query Match 57.8%; Score 48; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      7 PQVTRGDVF 15
          |||||||||
Db      2 pqvtrgdvf 10


RESULT   6
W66820
ID   W66820 standard; peptide; 9 AA.
XX
AC   W66820;
XX
DT   10-DEC-1998  (first entry)
XX
DE   Peptide used in purification of vitronectin receptor.
XX
KW   bone resorption; pharmacore; angiogenesis; restenosis; integrin receptor;
KW   alpha v beta 3 integrin receptor; osteoclast; vitronectin receptor;
KW   affinity chromatography.
XX
OS   Synthetic.
XX
PN   US5807819-A.
XX
PD   15-SEP-1998.
XX
PF   12-APR-1995;   94US-0421698.
XX
PR   12-APR-1995;   95US-0421698.
PR   15-APR-1994;   94US-0227316.
PR   08-SEP-1994;   94US-0303052.
XX
PA   (LJOL-) LA JOLLA CANCER RES CENT.
XX
PI   Cheng S,  Ingram R,  Mullen D,  Tschopp JF;
XX
DR   WPI; 1998-555601/47.
XX
PT   Use of peptide derivatives which can alter integrin receptor binding
PT   - for altering bone resorption, treating angiogenesis or restenosis
PT   and altering integrin receptor mediated interactions
XX
PS   Example 2; Column 22; 87pp; English.
XX
CC   The invention relates to peptides that are useful for inhibiting bone
CC   resorption, angiogenesis or restenosis, and for altering integrin
CC   receptor-mediated interactions, especially alpha v beta 3 integrin
CC   receptor-mediated binding of cells to a matrix. They may be used for
CC   reducing or inhibiting osteoclast binding to a matrix. Administration is
CC   oral, parenteral, topical, transdermal or by inhalation. The present
CC   sequence represents a peptide used in an affinity chromagraphy column for
CC   purification of the human alpha v beta 3 vitronectin receptor.
XX
SQ   Sequence   9 AA;

  Query Match             43.4%;  Score 36;  DB 19;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      9 VTRGDVF 15
          |||||||
Db      1 vtrgdvf 7


RESULT   7
W97014
ID   W97014 standard; peptide; 9 AA.
XX
AC   W97014;
XX
DT   26-APR-1999  (first entry)
XX
DE   Peptide used to inhibit bone resorption, angiogenesis and restenosis.
XX
KW   RGD-peptide; bone resorption; angiogenesis; restenosis;
KW   integrin receptor mediated interaction; binding; osteoclast; bone.
XX
OS   Synthetic.
XX
PN   US5849865-A.
XX
PD   15-DEC-1998.
XX
PF   12-APR-1995;   95US-0421695.
XX
PR   12-APR-1995;   95US-0421695.
PR   13-APR-1994;   94US-0227316.
PR   08-SEP-1994;   94US-0303052.
XX
PA   (LJOL-) LA JOLLA CANCER RES FOUND.
XX
PI   Cheng S,  Ingram R,  Mullen D,  Tschopp JF;
XX
DR   WPI; 1999-179486/15.
XX
PT   RGD peptides - that modulate integrin-mediated cell-matrix binding
XX
PS   Disclosure; Columns 35-36; 90pp; English.
XX
CC   The present peptide represents a non-naturally occurring
CC   Arg-Gly-Asp (RGD)-containing peptide. The peptide may be
CC   useful for reducing or inhibiting bone resorption, angiogenesis
CC   or restenosis, and for altering an integrin receptor mediated
CC   interaction. The peptide may also be used to inhibit the binding
CC   of an osteoclast to bone.
XX
SQ   Sequence   9 AA;

  Query Match             43.4%;  Score 36;  DB 20;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      9 VTRGDVF 15
          |||||||
Db      1 vtrgdvf 7


RESULT   8
W68121
ID   W68121 standard; peptide; 10 AA.
XX
AC   W68121;
XX
DT   30-SEP-1998  (first entry)
XX
DE   Human bone apposition peptide modified active fragment 11.
XX
KW   Bone stimulatory activity; BSA; bone growth; bone reduction disease;
KW   osteoporosis; bone apposition.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 8
FT                   /label= D8E
FT                   /note= "wild-type (W68109) Asp is replaced by Glu"
XX
PN   WO9826070-A1.
XX
PD   18-JUN-1998.
XX
PF   11-DEC-1997;   97WO-CA00967.
XX
```

PR 11-DEC-1996; 96US-0763458.
XX
PA (GENS-) GENSCI REGENERATION SCI INC.
XX
PI Tam CS;
XX
DR WPI; 1998-348527/30.
DR N-PSDB; V41207.
XX
PT New bone growth stimulating factors - used to develop products for
PT the diagnosis, prevention and treatment of bone reduction disease,
PT particularly osteoporosis
XX
PS Claim 35; Page 56; 82pp; English.
XX
CC This is a modified active fragment of the human bone apposition peptide
CC (W68101). Peptides derived from this sequence (W68101) can exhibit bone
CC stimulatory activity (BSA). The specification provides active peptide
CC sequences as shown in W68103 to W68109, W68117 to W68123 and W68129 to
CC W68133 which promote bone growth in mammals. These peptides have in vivo
CC BSA in mammals and increase the mineral content in bones. A vector
CC comprising a DNA sequence encoding the BSA activity exhibiting peptides
CC or their analogues can be used to recombinantly produce the polypeptides.
CC The polypeptides can be used for the stimulation of bone growth. They can
CC be used in the prevention and treatment of a bone reduction disease,
CC particularly osteoporosis. The products can also be used for detection
CC and diagnosis.
XX
SQ Sequence 10 AA;

Query Match 36.1%; Score 30; DB 19; Length 10;
Best Local Similarity 83.3%; Pred. No. 41;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTAECK 6
:|||||
Db 5 htaeck 10

RESULT 9
W68122
ID W68122 standard; peptide; 10 AA.
XX
AC W68122;
XX
DT 30-SEP-1998 (first entry)
XX
DE Human bone apposition peptide modified active fragment 12.
XX
KW Bone stimulatory activity; BSA; bone growth; bone reduction disease;
KW osteoporosis; bone apposition.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 3
FT /label= N3Q
FT /note= "wild-type (W68109) Asn is replaced by Gln"
FT Misc-difference 8
FT /label= D8E
FT /note= "wild-type (W68109) Asp is replaced by Glu"
XX
PN WO9826070-A1.
XX
PD 18-JUN-1998.
XX
PF 11-DEC-1997; 97WO-CA00967.
XX
PR 11-DEC-1996; 96US-0763458.
XX
PA (GENS-) GENSCI REGENERATION SCI INC.
XX
PI Tam CS;
XX
DR WPI; 1998-348527/30.
DR N-PSDB; V41208.
XX
PT New bone growth stimulating factors - used to develop products for
PT the diagnosis, prevention and treatment of bone reduction disease,
PT particularly osteoporosis
XX
PS Claim 35; Page 57; 82pp; English.
XX
CC This is a modified active fragment of the human bone apposition peptide
CC (W68101). Peptides derived from this sequence (W68101) can exhibit bone
CC stimulatory activity (BSA). The specification provides active peptide
CC sequences as shown in W68103 to W68109, W68117 to W68123 and W68129 to
CC W68133 which promote bone growth in mammals. These peptides have in vivo
CC BSA in mammals and increase the mineral content in bones. A vector
CC comprising a DNA sequence encoding the BSA activity exhibiting peptides
CC or their analogues can be used to recombinantly produce the polypeptides.
CC The polypeptides can be used for the stimulation of bone growth. They can
CC be used in the prevention and treatment of a bone reduction disease,
CC particularly osteoporosis. The products can also be used for detection
CC and diagnosis.
XX
SQ Sequence 10 AA;

Query Match 36.1%; Score 30; DB 19; Length 10;
Best Local Similarity 83.3%; Pred. No. 41;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTAECK 6
:|||||
Db 5 htaeck 10

RESULT 10
W68119
ID W68119 standard; peptide; 10 AA.
XX
AC W68119;
XX
DT 30-SEP-1998 (first entry)
XX
DE Human bone apposition peptide modified active fragment 9.
XX
KW Bone stimulatory activity; BSA; bone growth; bone reduction disease;
KW osteoporosis; bone apposition.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "N-terminal acetylation"
FT Misc-difference 3
FT /label= N3Q
FT /note= "wild-type (W68109) Asn is replaced by Gln"
FT Misc-difference 8
FT /label= D8E
FT /note= "wild-type (W68109) Asp is replaced by Glu"
FT Modified-site 10
FT /note= "C-terminal amide"
XX
PN WO9826070-A1.
XX
PD 18-JUN-1998.
XX
PF 11-DEC-1997; 97WO-CA00967.
XX
PR 11-DEC-1996; 96US-0763458.
XX

PA (GENS-) GENSCI REGENERATION SCI INC.
XX
PI Tam CS;
XX
DR WPI; 1998-348527/30.
XX
PT New bone growth stimulating factors - used to develop products for
PT the diagnosis, prevention and treatment of bone reduction disease,
PT particularly osteoporosis
XX
PS Claim 14; Page 32; 82pp; English.
XX
CC This is a modified active fragment of the human bone apposition peptide
CC (W68101). Peptides derived from this sequence (W68101) can exhibit bone
CC stimulatory activity (BSA). The specification provides active peptide
CC sequences as shown in W68103 to W68109, W68117 to W68123 and W68129 to
CC W68133 which promote bone growth in mammals. These peptides have in vivo
CC BSA in mammals and increase the mineral content in bones. A vector
CC comprising a DNA sequence encoding the BSA activity exhibiting peptides
CC or their analogues can be used to recombinantly produce the polypeptides.
CC The polypeptides can be used for the stimulation of bone growth. They can
CC be used in the prevention and treatment of a bone reduction disease,
CC particularly osteoporosis. The products can also be used for detection
CC and diagnosis.
XX
SQ Sequence 10 AA;

Query Match 36.1%; Score 30; DB 19; Length 10;
Best Local Similarity 83.3%; Pred. No. 41;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTAECK 6
:|||||
Db 5 htaeck 10

RESULT 11
R24067
ID R24067 standard; Protein; 11 AA.
XX
AC R24067;
XX
DT 27-NOV-1992 (first entry)
XX
DE Cell-to-cell binding inhibiting peptide subunit (6).
XX
KW Adhesion; integrin; multimer.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Cross-links 2..>11
FT /note= "multimers of sequence linked by interchain
FT disulfide bonds with Cys residues"
XX
PN WO9208476-A.
XX
PD 29-MAY-1992.
XX
PF 07-NOV-1991; 91WO-US08328.
XX
PR 07-NOV-1990; 90US-0610363.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Houghten RA, Ruggeri ZM;
XX
DR WPI; 1992-199940/24.
XX
PT Peptides inhibiting binding of adhesion mols. to cells expressing
PT integrins - for treating and preventing thrombus formation and
PT diseases associated with platelet aggregation
XX
PS Claim 67; Page 69; 70pp; English.
XX
CC A peptide which inhibits binding of adhesion mols. to cells
CC expressing integrins may comprise two subunits having the sequence
CC below, held together by an interchain stable bond. The sequence
CC RGD is in each of the subunits.
XX
SQ Sequence 11 AA;

Query Match 34.9%; Score 29; DB 13; Length 11;
Best Local Similarity 50.0%; Pred. No. 68;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CKPQVTRGDV 14
|: : :||||
Db 2 crrrrsrgdv 11

RESULT 12
R06020
ID R06020 standard; protein; 11 AA.
XX
AC R06020;
XX
DT 20-NOV-1990 (first entry)
XX
DE Oligopeptide, antigenic to N.menigitidis.
XX
KW Meningococcal disease; meningitis; vaccine;
KW Class I outer membrane protein; ds.
XX
OS Neisseria meningitidis.
XX
PN WO9006595-A.
XX
PD 28-JUN-1990.
XX
PF 19-DEC-1989; 89WO-US05678.
XX
PR 26-JUN-1989; 89NL-0001612.
PR 19-DEC-1988; 88NL-0003111.
PR 06-JAN-1989; 89NL-0000030.
PR 06-JAN-1989; 89NL-0000036.
XX
PA (PRAX-) PRAXIS BILOGICS IN.
PA (VOLK-) RIJKINSINSI VOLKSGEZONDH.
XX
PI SEID RC, PARADISO PR, POOLMAN JT, HOOGERHOUT P, WIERTZ EJ;
PI VANDERLEY P, HECKELS JE, CLARKE IN;
XX
DR WPI; 1990-224326/29.
XX
PT Meningococcus class 1 outer-membrane protein vaccine - useful to
PT immunise against meningococcal disease.
XX
PS Claim 50; Page 102; 120pp; English.
XX
CC Peptides derived from outer membrane, encoding homo/heterologous
CC product such as a antigen-flagelin fusion protein, are useful in
CC eliciting a strong and wide ranging immune response against most
CC serotypes.
XX
SQ Sequence 11 AA;

Query Match 33.7%; Score 28; DB 11; Length 11;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 KPQVTRG 12
:|||| |

```
Db      1 qpqvtng 7


RESULT  13
R76241
ID   R76241 standard; Peptide; 12 AA.
XX
AC   R76241;
XX
DT   06-NOV-1995  (first entry)
XX
DE   Human Fas peptide 147-152/174-179.
XX
KW   Fas-delta-TM; transmembrane deletion; apoptosis; antibody;
KW   adoptive immunotherapy; transgenic animal.
XX
OS   Synthetic.
XX
PN   WO9513701-A.
XX
PD   26-MAY-1995.
XX
PF   15-NOV-1994;   94WO-US13173.
XX
PR   15-NOV-1993;   93US-0152443.
XX
PA   (LXRB-) LXR BIOTECHNOLOGY INC.
XX
PI   Barr PJ,  Kiefer MC,  Shapiro JP;
XX
DR   WPI; 1995-200120/26.
XX
PT   New nucleic acid encoding Fas protein without its trans-membrane region
PT   - and related vectors, transformed cells, transgenic animals, protein and
PT   antibodies, useful for control of Fas mediated apoptosis
XX
PS   Disclosure; Fig.4; 38pp; English.
XX
CC   Synthetic peptides corresp. to the extracellular, transmembrane
CC   (TM) and truncated TM regions of fas proteins, given in R75239-41,
CC   respectively, were used to raise antibodies useful in detecting
CC   biologically important fas molecules.
XX
SQ   Sequence   12 AA;


  Query Match             33.7%;  Score 28;  DB 16;  Length 12;
  Best Local Similarity   45.5%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      4 ECKPQVTRGDV 14
          :|| :| | :|
Db      2 kckeevkrkev 12


RESULT  14
Y84806
ID   Y84806 standard; peptide; 12 AA.
XX
AC   Y84806;
XX
DT   08-AUG-2000  (first entry)
XX
DE   Internal peptide of tumour necrosis factor inhibitory protein B1.
XX
KW   Tumour necrosis factor; TNF; TNF inhibitory protein; TIP; TIP-B1;
KW   TNF-induced cell lysis; TNF-induced apoptosis; cytolytic; septic shock;
KW   chronic inflammation; arthritis; cancer; cachexia; autoimmune disease.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1
FT                   /note= "unspecified amino acid"
XX
PN   EP997475-A1.
XX
PD   03-MAY-2000.
XX
PF   04-DEC-1998;   98EP-0123140.
XX
PR   21-SEP-1998;   98US-0157910.
XX
PA   (HEAL-) HEALTH RES INC.
XX
PI   Berleth E,  Ehrke JM,  Nadadur S,  Gurtoo H,  Henn A,  Mihich E;
XX
DR   WPI; 2000-305801/27.
XX
PT   Tumour necrosis factor inhibitory protein B1 capable of inhibiting the
PT   action of tumor necrosis factor upon introduction into the
PT   extracellular region of cells, useful for treating e.g. chronic
PT   inflammation
XX
PS   Claim 2; Page 15; 47pp; English.
XX
CC   Y84804-06 represent internal peptides of a tumour necrosis factor
CC   (TNF) inhibitory protein (TIP) designated TIP-B1. The TIP-B1 protein
CC   has a molecular weight of 27 kD, and which, upon introduction into
CC   the extracellular region of surrounding cells, is capable of
CC   inhibiting the action of TNF upon those cells. TIP-B1 is useful
CC   for inhibiting the action of TNF upon a cell to ablate e.g.
CC   TNF-induced cell lysis, TNF-induced apoptosis and cytolytic effects.
CC   TIP-B1 can therefore be used to treat TNF-mediated diseases such
CC   as chronic inflammation, arthritis, cancer (cachexia), autoimmune
CC   diseases and septic shock.
XX
SQ   Sequence   12 AA;


  Query Match             33.7%;  Score 28;  DB 21;  Length 12;
  Best Local Similarity   44.4%;  Pred. No. 1.1e+02;
  Matches    4;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      7 PQVTRGDVF 15
          ||:  || :
Db      4 pgivngdqy 12


RESULT  15
R95959
ID   R95959 standard; peptide; 13 AA.
XX
AC   R95959;
XX
DT   08-AUG-1996  (first entry)
XX
DE   Heterologous protein N-terminal extension #24.
XX
KW   Signal peptide; alpha-factor; dipeptidyl aminopeptidase processing;
KW   proteolysis; yeast; aprotinin; tissue factor pathway inhibitor; ILGF-I;
KW   protease inhibitor; insulin-like growth factor I; ILGF-II; interleukin;
KW   human growth hormone; bovine growth hormone; glucagon-like peptide-1;
KW   tissue plasminogen activator; glucagon; Factor VII; Factor VIII; insulin;
KW   Factor XIII; platelet derived growth factor; insulin precursor.
XX
OS   Synthetic.
XX
PN   WO9535384-A1.
XX
PD   28-DEC-1995.
XX
PF   16-JUN-1995;   95WO-DK00250.
XX
PR   17-JUN-1994;   94DK-0000712.
XX
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PA (NOVO) NOVO-NORDISK AS.
XX
PI Brandt J, Kjeldsen TB, Vad K;
XX
DR WPI; 1996-058421/06.
XX
PT DNA construct for expressing N-terminally extended heterologous
PT protein in yeast - enabling higher yield of correctly processed
PT proteins such as growth hormone, interleukin, tissue plasminogen
PT activator and insulin
XX
PS Example 11; Page 28; 79pp; English.
XX
CC R87060-R87082 and R95959 represent possible N-terminal extensions for
CC heterologous proteins (HP) in yeast. The N-terminally expended HP has a
CC signal peptide (such as the alpha-factor signal peptide, see R87059), a
CC leader sequence and a yeast processing site attached to its N-terminus.
CC The DNA encoding this construct is then inserted into a recombinant
CC expression vector which is used to transform a yeast strain capable of
CC expressing the heterologous protein. The yeast processing site,
CC contained within the N-terminal extension, enables the leader sequence
CC and signal peptide to be removed. The N-terminal extension of the HP
CC increases the fermentation yield and protects against dipeptidyl
CC aminopeptidase processing. The extension can be cleaved off either by
CC naturally occurring yeast proteases before purification from the culture
CC media or by in vitro proteolysis during or subsequent to purification of
CC the product. These constructs can be used to obtain higher yields of
CC correctly processed proteins such as aprotinin, tissue factor pathway
CC inhibitor, protease inhibitors, insulin-like growth factor I (ILGF-I),
CC ILGF-II, human or bovine growth hormone, interleukin, tissue plasminogen
CC activator, glucagon, glucagon-like peptide-1, Factor VII, Factor VIII,
CC Factor XIII, platelet derived growth factor, enzymes, insulin, or an
CC insulin precursor.
XX
SQ Sequence 13 AA;

Query Match 33.7%; Score 28; DB 17; Length 13;
Best Local Similarity 55.6%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AECKPQVTR 11
|| :|: ||
Db 5 aeaepkatr 13

Search completed: March 6, 2001, 09:48:41
Job time: 163 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: March 6, 2001, 09:47:08 ; Search time 12.67 Seconds
(without alignments)
21.259 Million cell updates/sec

Title: US-09-081-522-8
Perfect score: 83
Sequence: 1 YTAECKPQVTRGDVF 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 78116

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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5: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	83	100.0	15	1	US-08-210-715-8	Sequence 8, Appli
2	83	100.0	15	1	US-08-366-665-8	Sequence 8, Appli
3	36	43.4	9	1	US-08-421-702A-6	Sequence 6, Appli
4	36	43.4	9	1	US-08-303-052A-6	Sequence 6, Appli
5	36	43.4	9	1	US-08-421-696A-6	Sequence 6, Appli
6	36	43.4	9	1	US-08-421-697A-6	Sequence 6, Appli
7	36	43.4	9	1	US-08-421-698A-6	Sequence 6, Appli
8	36	43.4	9	2	US-08-421-695A-6	Sequence 6, Appli
9	36	43.4	9	4	PCT-US95-04741-6	Sequence 6, Appli
10	30	36.1	10	3	US-08-763-458-28	Sequence 28, Appl
11	30	36.1	10	3	US-08-763-458-29	Sequence 29, Appl
12	29	34.9	11	4	PCT-US91-08328-10	Sequence 10, Appl
13	28	33.7	12	1	US-08-444-231-22	Sequence 22, Appl
14	28	33.7	12	1	US-08-152-443A-22	Sequence 22, Appl
15	27	32.5	8	1	US-08-014-426-54	Sequence 54, Appl
16	27	32.5	8	4	PCT-US94-01319-54	Sequence 54, Appl
17	27	32.5	8	5	5179198-5	Patent No. 5179198
18	27	32.5	8	5	5521296-5	Patent No. 5521296
19	27	32.5	10	3	US-08-763-458-9	Sequence 9, Appli
20	27	32.5	10	3	US-08-763-458-30	Sequence 30, Appl
21	27	32.5	11	2	US-08-487-074-14	Sequence 14, Appl
22	27	32.5	11	3	US-08-763-458-16	Sequence 16, Appl
23	27	32.5	14	1	US-08-325-071-70	Sequence 70, Appl
24	27	32.5	14	3	US-08-763-458-8	Sequence 8, Appli
25	27	32.5	15	2	US-08-487-074-7	Sequence 7, Appli
26	27	32.5	15	3	US-08-763-458-7	Sequence 7, Appli
27	26	31.3	9	1	US-08-421-702A-53	Sequence 53, Appl
28	26	31.3	9	1	US-08-421-702A-99	Sequence 99, Appl
29	26	31.3	9	1	US-08-303-052A-72	Sequence 72, Appl
30	26	31.3	9	1	US-08-303-052A-99	Sequence 99, Appl
31	26	31.3	9	1	US-08-421-696A-53	Sequence 53, Appl
32	26	31.3	9	1	US-08-421-696A-99	Sequence 99, Appl
33	26	31.3	9	1	US-08-421-697A-53	Sequence 53, Appl
34	26	31.3	9	1	US-08-421-697A-99	Sequence 99, Appl
35	26	31.3	9	1	US-08-421-698A-53	Sequence 53, Appl
36	26	31.3	9	1	US-08-421-698A-99	Sequence 99, Appl
37	26	31.3	9	2	US-08-421-695A-100	Sequence 100, App
38	26	31.3	9	2	US-08-421-695A-142	Sequence 142, App
39	26	31.3	10	1	US-08-710-305-1	Sequence 1, Appli
40	26	31.3	12	3	US-08-742-243-3	Sequence 3, Appli
41	26	31.3	12	3	US-08-742-243-65	Sequence 65, Appl
42	26	31.3	12	3	US-08-742-243-66	Sequence 66, Appl
43	26	31.3	12	3	US-08-742-243-67	Sequence 67, Appl
44	26	31.3	14	3	US-08-807-992B-9	Sequence 9, Appli
45	26	31.3	14	3	US-08-807-992B-12	Sequence 12, Appl

ALIGNMENTS

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RESULT 1
US-08-210-715-8
; Sequence 8, Application US/08210715
; Patent No. 5753230
; GENERAL INFORMATION:
;   APPLICANT: Brooks, Peter
;   APPLICANT: Cheresh, David A
;   TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR
;   TITLE OF INVENTION: INHIBITION OF ANGIOGENESIS
;   NUMBER OF SEQUENCES: 14
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Office of Patent Counsel, The Scripps
;     ADDRESSEE: Research Institute
;     STREET: 10665 No. 5753230th Torrey Pines Road, TPC-8
;     CITY: La Jolla
;     STATE: CA
;     COUNTRY: USA
;     ZIP: 92037
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/210,715
;     FILING DATE: 18-MAR-1994
;     CLASSIFICATION: 514
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Fitting, Thomas
;     REGISTRATION NUMBER: 34,163
;     REFERENCE/DOCKET NUMBER: TSRI 419.0
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (619) 554-2937
;     TELEFAX: (619) 554-6312
; INFORMATION FOR SEQ ID NO: 8:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 15 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   FRAGMENT TYPE: internal
US-08-210-715-8


  Query Match 100.0%; Score 83; DB 1; Length 15;
  Best Local Similarity 100.0%; Pred. No. 1.5e-07;
  Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 YTAECKPQVTRGDVF 15
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Db      1 YTAECKPQVTRGDVF 15


RESULT   2
US-08-366-665-8
; Sequence 8, Application US/08366665
; Patent No. 5766591
;  GENERAL INFORMATION:
;    APPLICANT:  Brooks, Peter
;    APPLICANT:  Cheresh, David A
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS USEFUL FOR
;    TITLE OF INVENTION:  INHIBITION OF ANGIOGENESIS
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Office of Patent Counsel, The Scripps
;      ADDRESSEE:  Research Institute
;      STREET:  10666 No. 5766591th Torrey Pines Road, TPC-8
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/366,665
;      FILING DATE:  30-DEC-1994
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/210,715
;      FILING DATE:  18-MAR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fitting, Thomas
;      REGISTRATION NUMBER:  34,163
;      REFERENCE/DOCKET NUMBER:  TSRI 419.1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 554-2937
;      TELEFAX:  (619) 554-6312
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  internal
US-08-366-665-8


  Query Match           100.0%;  Score 83;  DB 1;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 1.5e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 YTAECKPQVTRGDVF 15
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Db      1 YTAECKPQVTRGDVF 15


RESULT   3
US-08-421-702A-6
; Sequence 6, Application US/08421702A
; Patent No. 5759996
;  GENERAL INFORMATION:
;    APPLICANT:  Cheng, Soan
;    APPLICANT:  Ingram, Ronald
;    APPLICANT:  Mullen, Daniel
;    APPLICANT:  Tschopp, Juerg
;    TITLE OF INVENTION:  Peptides Useful for Altering Alpha-
;    TITLE OF INVENTION:  v Beta-3-Mediated Binding
;    NUMBER OF SEQUENCES:  140
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell & Flores LLP
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/421,702A
;      FILING DATE:  12-APR-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/303,052
;      FILING DATE:  08-SEP-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-LA 1480
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-421-702A-6


  Query Match           43.4%;  Score 36;  DB 1;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 1.3e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      9 VTRGDVF 15
          |||||||
Db      1 VTRGDVF 7


RESULT   4
US-08-303-052A-6
; Sequence 6, Application US/08303052A
; Patent No. 5770565
;  GENERAL INFORMATION:
;    APPLICANT:  Cheng, Soan
;    APPLICANT:  Ingram, Ronald
;    APPLICANT:  Mullen, Daniel
;    APPLICANT:  Tschopp, Juerg
;    TITLE OF INVENTION:  Peptides for Reducing or Inhibiting Bone
;    TITLE OF INVENTION:  Resorption
;    NUMBER OF SEQUENCES:  113
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell & Flores LLP
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/303,052A
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;      FILING DATE:  08-SEP-1994
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/227,316
;      FILING DATE:  13-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-LA 1132
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-303-052A-6


  Query Match           43.4%;  Score 36;  DB 1;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 1.3e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      9 VTRGDVF 15
          |||||||
Db      1 VTRGDVF 7


RESULT   5
US-08-421-696A-6
; Sequence 6, Application US/08421696A
; Patent No. 5773412
;  GENERAL INFORMATION:
;    APPLICANT:  Cheng, Soan
;    APPLICANT:  Ingram, Ronald
;    APPLICANT:  Mullen, Daniel
;    APPLICANT:  Tschopp, Juerg
;    TITLE OF INVENTION:  Use of Peptides for Altering alpha-v
;    TITLE OF INVENTION:  Beta-3-Mediated Binding
;    NUMBER OF SEQUENCES:  138
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell & Flores LLP
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/421,696A
;      FILING DATE:  12-APR-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/303,052
;      FILING DATE:  08-SEP-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-LA 1479
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-421-696A-6


  Query Match           43.4%;  Score 36;  DB 1;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 1.3e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      9 VTRGDVF 15
          |||||||
Db      1 VTRGDVF 7


RESULT   6
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; Sequence 5, Application US/08421697A
; Patent No. 5792745
;  GENERAL INFORMATION:
;    APPLICANT:  Cheng, Soan
;    APPLICANT:  Ingram, Ronald
;    APPLICANT:  Mullen, Daniel
;    APPLICANT:  Tschopp, Juerg
;    TITLE OF INVENTION:  Use of Peptides for Altering Bone
;    TITLE OF INVENTION:  Resorption
;    NUMBER OF SEQUENCES:  138
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell & Flores LLP
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/421,697A
;      FILING DATE:  12-APR-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/227,316
;      FILING DATE:  13-APR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/303,052
;      FILING DATE:  08-SEP-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-LA 1412
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-421-697A-6


  Query Match           43.4%;  Score 36;  DB 1;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 1.3e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      9 VTRGDVF 15
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Db      1 VTRGDVF 7


RESULT   7
US-08-421-698A-6
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; Sequence 6, Application US/08421698A
; Patent No. 5807819
;  GENERAL INFORMATION:
;    APPLICANT:  Cheng, Soan
;    APPLICANT:  Ingram, Ronald
;    APPLICANT:  Mullen, Daniel
;    APPLICANT:  Tschopp, Juerg
;    TITLE OF INVENTION:  Peptides Useful for Altering Bone
;    TITLE OF INVENTION:  Resorption
;    NUMBER OF SEQUENCES:  138
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell & Flores LLP
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/421,698A
;      FILING DATE:  12-APR-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/303,052
;      FILING DATE:  08-SEP-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-LA 1481
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-421-698A-6


  Query Match             43.4%;  Score 36;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       9 VTRGDVF 15
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Db       1 VTRGDVF 7


RESULT   8
US-08-421-695A-6
; Sequence 6, Application US/08421695A
; Patent No. 5849865
;  GENERAL INFORMATION:
;    APPLICANT:  Cheng, Soan
;    APPLICANT:  Ingram, Ronald
;    APPLICANT:  Mullen, Daniel
;    APPLICANT:  Tschopp, Juerg
;    TITLE OF INVENTION:  Peptides for Altering Bone Resorption,
;    TITLE OF INVENTION:  Angiogenesis and Restenosis
;    NUMBER OF SEQUENCES:  143
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell & Flores LLP
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/421,695A
;      FILING DATE:  12-APR-1995
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-LA 1478
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  peptide
US-08-421-695A-6


  Query Match             43.4%;  Score 36;  DB 2;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       9 VTRGDVF 15
           |||||||
Db       1 VTRGDVF 7


RESULT   9
PCT-US95-04741-6
; Sequence 6, Application PC/TUS9504741
;  GENERAL INFORMATION:
;    APPLICANT:  La Jolla Cancer Research Foundation
;    TITLE OF INVENTION:  Peptides for Reducing or Inhibiting Bone
;    TITLE OF INVENTION:  Resorption, Angiogenesis and Restenosis
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/04741
;      FILING DATE:  12-APR-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/227,316
;      FILING DATE:  13-APR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/303,052
;      FILING DATE:  08-SEP-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Imbra, Richard J.
;      REGISTRATION NUMBER:  37,643
;      REFERENCE/DOCKET NUMBER:  FP-LA 1476
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
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;      LENGTH:  9 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
PCT-US95-04741-6


  Query Match           43.4%;  Score 36;  DB 4;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 1.3e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      9 VTRGDVF 15
          |||||||
Db      1 VTRGDVF 7


RESULT  10
US-08-763-458-28
; Sequence 28, Application US/08763458
; Patent No. 6117839
;  GENERAL INFORMATION:
;    APPLICANT:  TAM, Cherk Shing
;    TITLE OF INVENTION:  BONE STIMULATING FACTOR
;    NUMBER OF SEQUENCES:  33
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/763,458
;      FILING DATE:  11-DEC-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/467,074
;      FILING DATE:  07-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEGNER, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  79997/118
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  28:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-763-458-28


  Query Match           36.1%;  Score 30;  DB 3;  Length 10;
  Best Local Similarity  83.3%;  Pred. No. 37;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 YTAECK 6
          :|||||
Db      5 HTAECK 10


RESULT  11
US-08-763-458-29
; Sequence 29, Application US/08763458
; Patent No. 6117839
;  GENERAL INFORMATION:
;    APPLICANT:  TAM, Cherk Shing
;    TITLE OF INVENTION:  BONE STIMULATING FACTOR
;    NUMBER OF SEQUENCES:  33
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/763,458
;      FILING DATE:  11-DEC-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/487,074
;      FILING DATE:  07-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEGNER, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  79997/118
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  29:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-763-458-29


  Query Match           36.1%;  Score 30;  DB 3;  Length 10;
  Best Local Similarity  83.3%;  Pred. No. 37;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 YTAECK 6
          :|||||
Db      5 HTAECK 10


RESULT  12
PCT-US91-08328-10
; Sequence 10, Application PC/TUS9108328
;  GENERAL INFORMATION:
;    APPLICANT:  Ruggeri, Zaverio M.
;    APPLICANT:  Houghten, Richard A.
;    TITLE OF INVENTION:  PEPTIDES THAT INHIBIT PLATELET BINDING
;    TITLE OF INVENTION:  OF ADHESION MOLECULES
;    NUMBER OF SEQUENCES:  47
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Eugene Moroz, MORGAN & FINNEGAN
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10154
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US91/08328
;      FILING DATE:  19911107
```

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;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/610,363
;       FILING DATE:  07-NOV-1990
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Moroz, Eugene
;       REGISTRATION NUMBER:  25,237
;       REFERENCE/DOCKET NUMBER:  1198 4079PC
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212)758-4800
;       TELEFAX:  (212)751-6849
;       TELEX:  421792
;   INFORMATION FOR SEQ ID NO:  10:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  11 amino acids
;       TYPE:  AMINO ACID
;       TOPOLOGY:  unknown
;     MOLECULE TYPE:  peptide
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     FEATURE:
;       NAME/KEY:  Cross-links
;       LOCATION:  2..>11
;       OTHER INFORMATION:  /note= "Multimers of sequence
;       OTHER INFORMATION:  linked by interchain disulfide bonds at Cys
;       OTHER INFORMATION:  residues"
;     PUBLICATION INFORMATION:
;       DOCUMENT NUMBER:  US 4,683,291
;       FILING DATE:  28-OCT-1985
;       PUBLICATION DATE:  28-JUL-1987
;     PUBLICATION INFORMATION:
;       DOCUMENT NUMBER:  US B1 4,683,291
;       FILING DATE:  28-OCT-1985
;       PUBLICATION DATE:  03-JUL-1990
PCT-US91-08328-10


  Query Match             34.9%;  Score 29;  DB 4;  Length 11;
  Best Local Similarity   50.0%;  Pred. No. 59;
  Matches    5;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       5 CKPQVTRGDV 14
           |: : :||||
Db       2 CRRRRSRGDV 11


RESULT  13
US-08-444-231-22
; Sequence 22, Application US/08444231
; Patent No. 5652210
;  GENERAL INFORMATION:
;    APPLICANT:  BARR, PHILIP J.
;    APPLICANT:  SHAPIRO, JOHN P.
;    APPLICANT:  KIEFER, MICHAEL C.
;    TITLE OF INVENTION:  NOVEL FAS PROTEIN AND METHODS OF USE
;    TITLE OF INVENTION:  THEREOF
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 Page Mill Road
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/444,231
;      FILING DATE:  18-MAY-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/152,443
;      FILING DATE:  15-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  LEHNHARDT, SUSAN K.
;      REGISTRATION NUMBER:  33,943
;      REFERENCE/DOCKET NUMBER:  23647-20006.00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 813-5600
;      TELEFAX:  (415) 494-0792
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-444-231-22


  Query Match             33.7%;  Score 28;  DB 1;  Length 12;
  Best Local Similarity   45.5%;  Pred. No. 93;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4 ECKPQVTRGDV 14
           :|| :| | :|
Db       2 KCKEEVKRKEV 12


RESULT  14
US-08-152-443A-22
; Sequence 22, Application US/08152443A
; Patent No. 5663070
;  GENERAL INFORMATION:
;    APPLICANT:  BARR, PHILIP J.
;    APPLICANT:  SHAPIRO, JOHN P.
;    APPLICANT:  KIEFER, MICHAEL C.
;    TITLE OF INVENTION:  NOVEL FAS PROTEIN AND METHODS OF USE
;    TITLE OF INVENTION:  THEREOF
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 Page Mill Road
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/152,443A
;      FILING DATE:  15-NOV-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  LEHNHARDT, SUSAN K.
;      REGISTRATION NUMBER:  33,943
;      REFERENCE/DOCKET NUMBER:  23647-20006.00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 813-5600
;      TELEFAX:  (415) 494-0792
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-152-443A-22
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```
  Query Match           33.7%;  Score 28;  DB 1;  Length 12;
  Best Local Similarity  45.5%;  Pred. No. 93;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4 ECKPQVTRGDV 14
           :|| :| | :|
Db       2 KCKEEVKRKEV 12


RESULT  15
US-08-014-426-54
; Sequence 54, Application US/08014426
; Patent No. 5512435
;  GENERAL INFORMATION:
;    APPLICANT:  Renschler, Markus F.
;    APPLICANT:  Levy, Ronald
;    APPLICANT:  Bhatt, Ramesh
;    APPLICANT:  Dower, William
;    TITLE OF INVENTION:  RECEPTOR-BINDING ANTIPROLIFERATIVE
;    TITLE OF INVENTION:  PEPTIDES
;    NUMBER OF SEQUENCES:  65
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  379 Lytton Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/014,426
;      FILING DATE:  05-FEB-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, Willaim M
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  5490A-204
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  54:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
US-08-014-426-54


  Query Match           32.5%;  Score 27;  DB 1;  Length 8;
  Best Local Similarity  66.7%;  Pred. No. 1.3e+05;
  Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 YTAECK 6
           :||:||
Db       2 WTADCK 7


Search completed: March  6, 2001, 09:48:57
Job time: 109 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: March 6, 2001, 09:47:33 ; Search time 13.92 Seconds
(without alignments)
73.169 Million cell updates/sec

Title: US-09-081-522-8
Perfect score: 83
Sequence: 1 YTAECKPQVTRGDVF 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_66:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	33	39.8	11	2	S42449	ant1 prctein - pha
2	25	30.1	9	2	B46250	alpha-adaptin - bo
3	22	26.5	10	1	RHLMGS	gonadoliberin - se
4	22	26.5	10	2	S70721	heat shock protein
5	22	26.5	14	2	PH0765	T-cell receptor be
6	21.5	25.9	15	2	A35389	urease (EC 3.5.1.5
7	21	25.3	11	2	S66606	quinoline 2-oxidor
8	21	25.3	12	2	PH1587	Ig H chain V-D-J r
9	21	25.3	14	2	PC7075	guanylate cyclase
10	21	25.3	15	2	PQ0017	terminal protein -
11	21	25.3	15	2	A60763	endo-1,3-beta-gluc
12	20	24.1	11	2	S60354	retinal oxidase -
13	20	24.1	12	1	UOGM2	urotensin II - lon
14	20	24.1	12	2	S42765	urotensin II - tel
15	20	24.1	14	2	PC4271	unidentified QR310
16	20	24.1	15	2	A28497	neurotensin-relate
17	20	24.1	15	2	C61511	milk band B protei
18	20	24.1	15	2	S08301	epidermal growth f
19	20	24.1	15	4	I38031	hypothetical MN1/T
20	19	22.9	9	2	G58502	kidney and bladder
21	19	22.9	13	2	A61210	antibiotic GE2270
22	19	22.9	14	2	PH1594	Ig H chain V-D-J r
23	19	22.9	15	2	I78838	flt3 ligand isofor
24	18	21.7	7	4	I55382	hypothetical pepti
25	18	21.7	11	2	S45386	low density lipopr
26	18	21.7	14	2	S39932	S-allele-associate
27	18	21.7	14	2	B61309	lutropin beta chai
28	18	21.7	15	2	S68731	bleomycin-binding
29	18	21.7	15	2	PA0088	protein QF200051 -
30	18	21.7	15	2	S29487	GTP-binding protei
31	17	20.5	8	2	I57532	gene TnIslow prote
32	17	20.5	10	1	XAVI6B	angiotensin-conver
33	17	20.5	10	2	S66214	cartilage oligomer
34	17	20.5	11	1	SPHO	substance P - hors
35	17	20.5	11	1	A60654	substance P - guin
36	17	20.5	11	2	S66196	alcohol dehydrogen
37	17	20.5	11	2	C37196	bradykinin-potenti
38	17	20.5	11	2	D37196	bradykinin-potenti
39	17	20.5	12	2	A60757	enterotoxin C-1 -
40	17	20.5	13	1	JTJG3	tremerogen a-13 -
41	17	20.5	13	2	I50173	alpha-2 collagen -
42	17	20.5	14	2	S33803	chaperone, TCP1-re
43	17	20.5	14	2	S23376	collagen alpha cha
44	17	20.5	14	2	A23996	beta-granin - rat
45	17	20.5	15	2	A56963	acid phosphatase (

ALIGNMENTS

RESULT 1
S42449
ant1 protein - phage P7
C;Species: phage P7
C;Date: 07-Sep-1994 #sequence_revision 26-May-1995 #text_change 08-Oct-1999
C;Accession: S42449
R;Citron, M.; Schuster, H.
Cell 62, 591-598, 1990
A;Title: The c4 repressors of bacteriophages P1 and P7 are antisense RNAs.
A;Reference number: S42448; MUID:90335968
A;Accession: S42449
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-11 <CIT>
A;Cross-references: EMBL:M35139; NID:g215705; PIDN:AAA32437.1; PID:g215707

Query Match 39.8%; Score 33; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy      6 KPQVTRGDV 14
          || ||| |:
Db      3 KPLVTRNDI 11
```

RESULT 2
B46250
alpha-adaptin - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 05-Apr-1995
C;Accession: B46250
R;Timerman, A.P.; Mayrleitner, M.M.; Lukas, T.J.; Chadwick, C.C.; Saito, A.; Wattersc
Proc. Natl. Acad. Sci. U.S.A. 89, 8976-8980, 1992
A;Title: Inositol polyphosphate receptor and clathrin assembly protein AP-2 are relat
A;Reference number: A46250; MUID:93028388
A;Accession: B46250
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <TIM>

Query Match 30.1%; Score 25; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 2e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy      7 PQVTRGD 13
          | |::||
Db      1 PAVSKGD 7
```

RESULT 3

```
RHLMGS
gonadoliberin - sea lamprey
N;Alternate names: gonadotropin releasing hormone (GnRH)
C;Species: Petromyzon marinus (sea lamprey)
C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 18-Mar-1997
C;Accession: A01412
R;Sherwood, N.M.; Sower, S.A.; Marshak, D.R.; Fraser, B.A.; Brownstein, M.J.
J. Biol. Chem. 261, 4812-4819, 1986
A;Title: Primary structure of gonadotropin-releasing hormone from lamprey brain.
A;Reference number: A01412; MUID:86158192
A;Accession: A01412
A;Molecule type: protein
A;Residues: 1-10 <SHE>
C;Comment: This hormone was isolated from the brain.
C;Superfamily: gonadoliberin
C;Keywords: amidated carboxyl end; hormone; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;10/Modified site: amidated carboxyl end (Gly) #status experimental


  Query Match           26.5%;  Score 22;  DB 1;  Length 10;
  Best Local Similarity  57.1%;  Pred. No. 9.5e+02;
  Matches    4;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 YTAECKP 7
          |: | ||
Db      3 YSLEWKP 9


RESULT   4
S70721
heat shock protein C62.5 homolog - Salmonella typhimurium (fragment)
N;Alternate names: high temperature protein G
C;Species: Salmonella typhimurium
C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 17-Apr-1998
C;Accession: S70721
R;Qi, S.Y.; Li, Y.; Szyroki, A.; Giles, I.G.; Moir, A.; O'Connor, C.D.
Mol. Microbiol. 17, 523-531, 1995
A;Title: Salmonella typhimurium responses to a bactericidal protein from human neutrophi
A;Reference number: S70719; MUID:96100451
A;Accession: S70721
A;Molecule type: protein
A;Residues: 1-10 <QIS>
A;Experimental source: strain SL1344
C;Keywords: ATP binding; heat shock; molecular chaperone


  Query Match           26.5%;  Score 22;  DB 2;  Length 10;
  Best Local Similarity  71.4%;  Pred. No. 9.5e+02;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      6 KPQVTRG 12
          | | |||
Db      2 KGQETRG 8


RESULT   5
PH0765
T-cell receptor beta chain (H1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C;Accession: PH0765
R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A;Title: T cell receptor genes in a series of class I major histocompatibility complex-r
allelic exclusion and antigen-specific repertoire.
A;Reference number: PH0746; MUID:92078846
A;Accession: PH0765
A;Molecule type: mRNA
A;Residues: 1-14 <CAS>
A;Cross-references: EMBL:X60859; NID:g51139; PIDN:CAA43249.1; PID:g51140
A;Experimental source: T lymphocyte
C;Keywords: T-cell receptor


  Query Match           26.5%;  Score 22;  DB 2;  Length 14;
  Best Local Similarity  44.4%;  Pred. No. 1.3e+03;
  Matches    4;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy      5 CKPQVTRGD 13
          |      |||
Db      1 CASSSARGD 9


RESULT   6
A35389
urease (EC 3.5.1.5) 63K chain - Morganella morganii (fragment)
C;Species: Morganella morganii
C;Date: 31-Aug-1990 #sequence_revision 31-Aug-1990 #text_change 23-Jun-1993
C;Accession: A35389
R;Hu, L.T.; Nicholson, E.B.; Jones, B.D.; Lynch, M.J.; Mobley, H.L.T.
J. Bacteriol. 172, 3073-3080, 1990
A;Title: Morganella morganii urease: purification, characterization, and isolation of
A;Reference number: A35389; MUID:90264298
A;Accession: A35389
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <HUA>
C;Keywords: hydrolase


  Query Match           25.9%;  Score 21.5;  DB 2;  Length 15;
  Best Local Similarity  41.7%;  Pred. No. 1.7e+03;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    3;  Gaps    1;

Qy      7 PQVTR---GDVF 15
          ||::|   | :|
Db      1 PQISRQEYGGLF 12


RESULT   7
S66606
quinoline 2-oxidoreductase alpha chain - Comamonas testosteroni (fragment)
C;Species: Comamonas testosteroni
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C;Accession: S66606
R;Schach, S.; Tshisuaka, B.; Fetzner, S.; Lingens, F.
Eur. J. Biochem. 232, 536-544, 1995
A;Title: Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-dioxygenase fr
A;Reference number: S66606; MUID:96035889
A;Accession: S66606
A;Molecule type: protein
A;Residues: 1-11 <SCH>
A;Experimental source: strain 63


  Query Match           25.3%;  Score 21;  DB 2;  Length 11;
  Best Local Similarity  66.7%;  Pred. No. 1.6e+03;
  Matches    4;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      3 AECKPQ 8
          || ||:
Db      6 AELKPR 11


RESULT   8
PH1587
Ig H chain V-D-J region (wild-type clone 11) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1587
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less m
A;Reference number: PH1580; MUID:93301609
A;Accession: PH1587
```

A;Molecule type: DNA
A;Residues: 1-12 <LEV>
A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin

Query Match 25.3%; Score 21; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
Qy      11 RGDVF 15
           |||::
Db       4 RGDLY 8
```

RESULT 9
PC7075
guanylate cyclase (EC 4.6.1.2), soluble, alpha-1 chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C;Accession: PC7075
R;Tsugita, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Matsui, T.; Watanabe, Y.;
Electrophoresis 21, 1853-1871, 2000
A;Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles of t
A;Reference number: PC7072
A;Accession: PC7075
A;Molecule type: protein
A;Residues: 1-14 <TSU>
A;Experimental source: strain C57BL/6Cr Slc, male; brain, striatum
C;Keywords: brain; phosphorus-oxygen lyase

Query Match 25.3%; Score 21; DB 2; Length 14;
Best Local Similarity 42.9%; Pred. No. 2e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

```
Qy       9 VTRGDVF 15
           : :|:||
Db       8 IPQGEVF 14
```

RESULT 10
PQ0017
terminal protein - phage M2 (fragment)
C;Species: phage M2
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Sep-1999
C;Accession: PQ0017
R;Matsumoto, K.; Takano, H.; Kim, C.I.; Hirokawa, H.
Gene 84, 247-255, 1989
A;Title: Primary structure of bactericphage M2 DNA polymerase: conserved segments within
A;Reference number: JQ0161; MUID:90128268
A;Accession: PQ0017
A;Molecule type: DNA
A;Residues: 1-15 <MAT>
A;Cross-references: GB:M33144; NID:g215507; PIDN:AAA32367.1; PID:g215508
C;Genetics:
A;Gene: E
C;Superfamily: phage PZA terminal protein

Query Match 25.3%; Score 21; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      11 RGDV 14
           ||||
Db       5 RGDV 8
```

RESULT 11
A60763
endo-1,3-beta-glucanase (EC 3.2.1.-), 68k - Bacillus circulans (strain WL-12) (fragment)
C;Species: Bacillus circulans
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 07-May-1999
C;Accession: A60753
R;Fiske, M.J.; Tobey-Fincher, K.L.; Fuchs, R.L.
J. Gen. Microbiol. 136, 2377-2383, 1990
A;Title: Cloning of two genes from Bacillus circulans WL-12 which encode 1,3-beta-glu
A;Reference number: A60763; MUID:91178514
A;Accession: A60763
A;Molecule type: protein
A;Residues: 1-15 <FIS>
C;Comment: This bacillus produces up to six different 1,3-beta-glucanases for growth
C;Keywords: glycosidase; hydrolase

Query Match 25.3%; Score 21; DB 2; Length 15;
Best Local Similarity 44.4%; Pred. No. 2.1e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```
Qy       7 PQVTRGDVF 15
           |:||  : |
Db       3 PEVTSMEYF 11
```

RESULT 12
S60354
retinal oxidase - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C;Accession: S60354
R;Huang, D.Y.; Ichikawa, Y.
Biochim. Biophys. Acta 1243, 431-436, 1995
A;Title: Identification of essential lysyl and cysteinyl residues, and the amino acid
A;Reference number: S60354; MUID:95244596
A;Accession: S60354
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <HUA>

Query Match 24.1%; Score 20; DB 2; Length 11;
Best Local Similarity 42.9%; Pred. No. 2.3e+03;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```
Qy       1 YTAECKP 7
           :|  | |
Db       5 HTXGCXP 11
```

RESULT 13
UOGM2
urotensin II - long-jawed mudsucker
C;Species: Gillichthys mirabilis (long-jawed mudsucker)
C;Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 15-Oct-1996
C;Accession: A01409
R;Pearson, D.; Shively, J.E.; Clark, B.R.; Geschwind, I.I.; Barkley, M.; Nishioka, R.
Proc. Natl. Acad. Sci. U.S.A. 77, 5021-5024, 1980
A;Title: Urotensin II: a somatostatin-like peptide in the caudal neurosecretory syste
A;Reference number: A01409; MUID:81054904
A;Accession: A01409
A;Molecule type: protein
A;Residues: 1-12 <PEA>
A;Note: the proposed sequence was confirmed by synthesis of a peptide with the same s
C;Comment: Urotensin II is found in the teleost caudal neurosecretory system and is i
C;Superfamily: urotensin II
C;Keywords: neuropeptide; osmoregulation
F;6-11/Disulfide bonds: #status experimental

Query Match 24.1%; Score 20; DB 1; Length 12;
Best Local Similarity 75.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy       2 TAEC 5
           ||:|
```

```
Db      3 TADC 6


RESULT  14
S42765
urotensin II - telostean fish
C;Species: telostean fish
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 05-Dec-1997
C;Accession: S42765
R;Bhaskaran, R.; Arunkumar, A.I.; Yu, C.
Biochim. Biophys. Acta 1199, 115-122, 1994
A;Title: NMR and dynamical simulated annealing studies on the solution conformation of u
A;Reference number: S42765; MUID:94169160
A;Accession: S42765
A;Molecule type: protein
A;Residues: 1-12 <BHA>
C;Superfamily: urotensin II
C;Keywords: neuropeptide; osmoregulation
F;6-11/Product: urotensin II #status experimental <MAT>


  Query Match             24.1%;  Score 20;  DB 2;  Length 12;
  Best Local Similarity   75.0%;  Pred. No. 2.5e+03;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 TAEC 5
          ||:|
Db      3 TADC 6


RESULT  15
PC4271
unidentified QR310007 protein - rice (fragment)
C;Species: Oryza sativa (rice)
C;Date: 28-May-1997 #sequence_revision 18-Jul-1997 #text_change 18-Jul-1997
C;Accession: PC4271
R;Kawakami, T.; Kamo, M.; Chen, M.C.; Tsugita, A.
submitted to JIPID, April 1997
A;Reference number: PC4267
A;Accession: PC4271
A;Molecule type: protein
A;Residues: 1-14 <KAW>


  Query Match             24.1%;  Score 20;  DB 2;  Length 14;
  Best Local Similarity   57.1%;  Pred. No. 2.9e+03;
  Matches    4;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      7 PQVTRGD 13
          | :| ||
Db      1 PGLTIGD 7


Search completed: March  6, 2001, 09:49:16
Job time: 103 sec
```

GenCore version 4.5

OM protein - protein search, using sw model

Run on: March 6, 2001, 09:48:43 ; Search time 8.42 Seconds
(without alignments)
57.531 Million cell updates/sec

Title: US-09-081-522-8
Perfect score: 83
Sequence: 1 YTAECKPQVTRGDVF 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 705

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	25	30.1	15	1	UC19_MAIZE	P80625 zea mays (m
2	22	26.5	10	1	GON1_PETMA	P04378 petromyzon
3	22	26.5	13	1	YPE2_LACLC	P42021 lactococcus
4	21.5	25.9	15	1	URE1_MORMO	P17337 morganella
5	21	25.3	11	1	Q2OA_COMTE	P80464 comamonas t
6	21	25.3	15	1	TERM_BPM2	P19897 bacteriopha
7	20	24.1	12	1	UR2_GILMI	P01147 gillichthys
8	20	24.1	12	1	UR2_POLSP	P81022 polyodon sp
9	20	24.1	13	1	UN02_PINPS	P81667 pinus pinas
10	19	22.9	9	1	RS11_SALTY	O54296 salmonella
11	19	22.9	13	1	PEDI_HYDAT	P80578 hydra atten
12	17.5	21.1	9	1	OXYT_RAJCL	P42994 raja clavat
13	17	20.5	10	1	BPP2_BOTJA	P01022 bothrops ja
14	17	20.5	11	1	BPP3_BOTIN	P30423 bothrops in
15	17	20.5	11	1	BPP4_BOTIN	P30424 bothrops in
16	17	20.5	11	1	TKNA_HORSE	P01290 equus cabal
17	17	20.5	13	1	TA13_TREME	P01370 tremella me
18	17	20.5	13	1	UN12_CLOPA	P81353 clostridium
19	17	20.5	14	1	TAT_HV1W2	P12509 human immun
20	17	20.5	14	1	TAT_HV1Z8	P12511 human immun
21	17	20.5	15	1	CBPB_PROAT	P19628 protopterus
22	17	20.5	15	1	CXA1_CONGE	P01519 conus geogr
23	16	19.3	7	1	FAR1_HELTI	P41871 helisoma tr
24	16	19.3	9	1	ISOT_CYPCA	P42993 cyprinus ca
25	16	19.3	9	1	UPA6_HUMAN	P30092 homo sapien
26	16	19.3	10	1	TKS1_AEDAE	P42634 aedes aegyp
27	16	19.3	10	1	TKS2_AEDAE	P42635 aedes aegyp
28	16	19.3	11	1	CORZ_PERAM	P11496 periplaneta
29	16	19.3	13	1	CXA1_CONST	P15471 conus stria
30	16	19.3	14	1	SMS1_MYOSC	P20750 myoxocephal
31	16	19.3	14	1	SMS_ALLMI	P31885 alligator m
32	16	19.3	15	1	ESTB_SCHGA	P81011 schizaphis
33	16	19.3	15	1	UC30_MAIZE	P80636 zea mays (m
34	15	18.1	7	1	FAR4_PANRE	P41875 panagrellus
35	15	18.1	10	1	AMPN_HELAM	P81731 helicoverpa
36	15	18.1	10	1	BPP2_BOTIN	P30422 bothrops in
37	15	18.1	10	1	FARP_MYTED	P42560 mytilus edu
38	15	18.1	10	1	UHA3_HUMAN	P40930 homo sapien
39	15	18.1	10	1	UPA5_HUMAN	P30091 homo sapien
40	15	18.1	12	1	TKN_KASSE	P08611 kassina sen
41	15	18.1	12	1	UR2A_CATCO	P04558 catostomus
42	15	18.1	12	1	V14K_WSSV	P82006 white spot
43	15	18.1	13	1	CXA2_CONGE	P01520 conus geogr
44	15	18.1	13	1	CXAA_CONST	P28878 conus stria
45	15	18.1	14	1	CXA1_CONCN	P56973 conus conso

ALIGNMENTS

RESULT 1
UC19_MAIZE
ID UC19_MAIZE STANDARD; PRT; 15 AA.
AC P80625;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE UNKNOWN PROTEIN FROM 2D-PAGE OF ETIOLATED COLEOPTILE (SPOT 406)
DE (FRAGMENT).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
RN [1]
RP SEQUENCE.
RC TISSUE=COLEOPTILE;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.6, ITS MW IS: 18.4 KDA.
DR MAIZE-2DPAGE; P80625; COLEOPTILE.
DR MAIZEDB; 123951; -.
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1672 MW; 1CF69D4DA8737F9D CRC64;

Query Match 30.1%; Score 25; DB 1; Length 15;
Best Local Similarity 55.6%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy       2 TAECKPQVT 10
           |  | | | ||
Db       7 TYGCSPPVT 15
```

RESULT 2
GON1_PETMA
ID GON1_PETMA STANDARD; PRT; 10 AA.
AC P04378;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE GONADOLIBERIN I (GONADOTROPIN-RELEASING HORMONE I) (GNRH-I)
DE (LULIBERIN I).
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Petromyzon.
RN [1]
RP SEQUENCE.
RC TISSUE=BRAIN;
RX MEDLINE=86168192; PubMed=3514603;
RA Sherwood N.M., Sower S.A., Marshak D.R., Fraser B.A., Brownstein M.J.;
RT "Primary structure of gonadotropin-releasing hormone from lamprey

```
RT   brain.";
RL   J. Biol. Chem. 261:4812-4819(1986).
CC   -!- FUNCTION: STIMULATES THE SECRETION OF BOTH LUTEINIZING AND
CC       FOLLICLE-STIMULATING HORMONES.
CC   -!- SIMILARITY: BELONGS TO THE GNRH FAMILY.
DR   PIR; A01412; RHLMGS.
DR   INTERPRO; IPR002012; -.
DR   PFAM; PF00446; GnRH; 1.
DR   PROSITE; PS00473; GNRH; 1.
KW   Hormone; Amidation; Hypothalamus.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES      10     10       AMIDATION.
SQ   SEQUENCE   10 AA;  1244 MW;  1E4B36237B1735AB CRC64;


  Query Match             26.5%;  Score 22;  DB 1;  Length 10;
  Best Local Similarity   57.1%;  Pred. No. 3.7e+02;
  Matches    4;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 YTAECKP 7
          |: | ||
Db      3 YSLEWKP 9


RESULT   3
YPE2_LACLC
ID   YPE2_LACLC     STANDARD;      PRT;    13 AA.
AC   P42021;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   01-NOV-1995 (Rel. 32, Last annotation update)
DE   HYPOTHETICAL PROTEIN IN PEPT 5'REGION (ORF2) (FRAGMENT).
OS   Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC   Lactococcus.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94245610; PubMed=8188586;
RA   Mierau I., Haandrikman A.J., Velterop O., Tan P.S.T., Leenhouts K.L.,
RA   Konings W.N., Venema G., Kok J.;
RT   "Tripeptidase gene (pepT) of Lactococcus lactis: molecular cloning
RT   and nucleotide sequencing of pepT and construction of a chromosomal
RT   deletion mutant.";
RL   J. Bacteriol. 176:2854-2861(1994).
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L27596; AAA20625.1; -.
KW   Hypothetical protein.
FT   NON_TER       1      1
SQ   SEQUENCE   13 AA;  1392 MW;  3671D53271B459D7 CRC64;


  Query Match             26.5%;  Score 22;  DB 1;  Length 13;
  Best Local Similarity   33.3%;  Pred. No. 4.8e+02;
  Matches    4;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy      2 TAECKPQVTRGD 13
          |   :| :: ||
Db      1 TTAIEPFISLGD 12


RESULT   4
URE1_MORMO
ID   URE1_MORMO     STANDARD;      PRT;    15 AA.
AC   P17337;
DT   01-AUG-1990 (Rel. 15, Created)
DT   01-AUG-1990 (Rel. 15, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   UREASE ALPHA SUBUNIT (EC 3.5.1.5) (UREA AMIDOHYDROLASE) (UREASE 63 KDA
DE   SUBUNIT) (FRAGMENT).
GN   UREC.
OS   Morganella morganii (Proteus morganii).
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Morganella.
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=90254298; PubMed=2345135;
RA   Hu L.-T., Nicholson E.B., Jones B.D., Lynch M.J., Mobley H.L.T.;
RT   "Morganella morganii urease: purification, characterization, and
RT   isolation of gene sequences.";
RL   J. Bacteriol. 172:3073-3080(1990).
CC   -!- CATALYTIC ACTIVITY: UREA + H(2)O = CO(2) + 2 NH(3).
CC   -!- COFACTOR: EACH CHAIN BINDS TWO NICKEL IONS.
CC   -!- SUBUNIT: (ALPHA, BETA, GAMMA)(3) (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE UREASE FAMILY.
DR   PIR; A35389; A35389.
DR   INTERPRO; IPR001924; -.
DR   PROSITE; PS00145; UREASE_2; PARTIAL.
DR   PROSITE; PS01120; UREASE_1; PARTIAL.
KW   Hydrolase; Metal-binding; Nickel.
FT   NON_TER      15     15
SQ   SEQUENCE   15 AA;  1550 MW;  09E27AA54241687B CRC64;


  Query Match             25.9%;  Score 21.5;  DB 1;  Length 15;
  Best Local Similarity   41.7%;  Pred. No. 6.9e+02;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    3;  Gaps    1;

Qy      7 PQVTR---GDVF 15
          ||:::|   | :|
Db      1 PQISRQEYGGLF 12


RESULT   5
Q2OA_COMTE
ID   Q2OA_COMTE     STANDARD;      PRT;    11 AA.
AC   P80464;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   01-FEB-1996 (Rel. 33, Last annotation update)
DE   QUINOLINE 2-OXIDOREDUCTASE, ALPHA CHAIN (EC 1.-.-.-) (FRAGMENT).
OS   Comamonas testosteroni (Pseudomonas testosteroni).
OC   Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; Comamonas.
RN   [1]
RP   SEQUENCE.
RC   STRAIN=63;
RX   MEDLINE=96035889; PubMed=7556204;
RA   Schach S., Tshisuaka B., Fetzner S., Lingens F.;
RT   "Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-
RT   dioxygenase from Comamonas testosteroni 63. The first two enzymes in
RT   quinoline and 3-methylquinoline degradation.";
RL   Eur. J. Biochem. 232:536-544(1995).
CC   -!- FUNCTION: CONVERTS (3-METHYL-)-QUINOLINE TO (3-METHYL-)2-OXO-
CC       1,2-DIHYDROQUINOLINE.
CC   -!- COFACTOR: FAD AND MOLYBDENUM.
CC   -!- PATHWAY: FIRST STEP IN THE DEGRADATION OF QUINOLINE AND
CC       (3-METHYL-)QUINOLINE.
CC   -!- SUBUNIT: HETEROHEXAMER OF TWO ALPHA CHAINS, TWO BETA CHAINS, AND
CC       TWO GAMMA CHAINS (PROBABLE).
KW   Oxidoreductase; Flavoprotein; FAD; Molybdenum.
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1213 MW;  869094322B1DC2CA CRC64;


  Query Match             25.3%;  Score 21;  DB 1;  Length 11;
  Best Local Similarity   66.7%;  Pred. No. 6.2e+02;
  Matches    4;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      3 AECKPQ 8
```

```
          || ||:
Db      6 AELKPR 11


RESULT   6
TERM_BPM2
ID   TERM_BPM2      STANDARD;      PRT;    15 AA.
AC   P19897;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   DNA TERMINAL PROTEIN (PROTEIN GP3) (FRAGMENT).
GN   3 OR E.
OS   Bacteriophage M2.
OC   Viruses; dsDNA viruses, no RNA stage; Tailed phages; Podoviridae.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90128268; PubMed=2515115;
RA   Matsumoto K., Takano H., Kim C.I., Hirokawa H.;
RT   "Primary structure of bacteriophage M2 DNA polymerase: conserved
RT   segments within protein-priming DNA polymerases and DNA polymerase I
RT   of Escherichia coli.";
RL   Gene 84:247-255(1989).
CC   -!- FUNCTION: DNA TERMINAL PROTEIN IS LINKED TO THE 5' ENDS OF
CC       BOTH STRANDS OF THE GENOME THROUGH A PHOSPHODIESTER BCND BETWEEN
CC       THE BETA-HYDROXYL GROUP OF A SERINE RESIDUE AND THE 5'-PHOSPHATE
CC       OF THE TERMINAL DEOXYADENYLATE. THIS PROTEIN IS ESSENTIAL FOR DNA
CC       REPLICATION AND IS INVOLVED IN THE PRIMING OF DNA ELONGATION.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M33144; AAA32367.1; -.
DR   PIR; PQ0017; PQ0017.
KW   Early protein; DNA replication; DNA priming;
KW   Covalent protein-DNA linkage.
FT   NON_TER       1      1
FT   SITE          5      7       CELL ATTACHMENT SITE (POTENTIAL).
SQ   SEQUENCE   15 AA;  1797 MW;  D3CBAFF8759DEA06 CRC64;


  Query Match             25.3%;  Score 21;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 8.5e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      11 RGDV 14
           ||||
Db       5 RGDV 8


RESULT   7
UR2_GILMI
ID   UR2_GILMI      STANDARD;      PRT;    12 AA.
AC   P01147;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   01-OCT-2000 (Rel. 40, Last annotation update)
DE   UROTENSIN II (U-II) (UII).
OS   Gillichthys mirabilis (Long-jawed mudsucker).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Gobioidei;
OC   Gobiidae; Gillichthys.
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=81054904; PubMed=6107911;
RA   Pearson D., Shively J.E., Clark B.R., Geschwind I.I., Barkley M.,
RA   Nishioka R., Bern H.A.;
RT   "Urotensin II: a somatostatin-like peptide in the caudal
RT   neurosecretory system of fishes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 77:5021-5024(1980).
CC   -!- FUNCTION: UROTENSIN IS FOUND IN THE TELEOST CAUDAL NEUROSECRETORY
CC       SYSTEM. IT HAS A SUGGESTED ROLE IN OSMOREGULATION AND AS A
CC       CORTICOTROPIN-RELEASING FACTOR.
CC   -!- SIMILARITY: BELONGS TO THE UROTENSIN 2 FAMILY.
DR   PIR; A01409; UOGM2.
DR   INTERPRO; IPR001483; -.
DR   PFAM; PF02083; Urotensin_II; 1.
DR   PROSITE; PS00984; UROTENSIN_II; 1.
KW   Hormone.
FT   DISULFID      6     11
SQ   SEQUENCE   12 AA;  1364 MW;  968BF8982679CEBA CRC64;


  Query Match             24.1%;  Score 20;  DB 1;  Length 12;
  Best Local Similarity   75.0%;  Pred. No. 1e+03;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 TAEC 5
            ||:|
Db       3 TADC 6


RESULT   8
UR2_POLSP
ID   UR2_POLSP      STANDARD;      PRT;    12 AA.
AC   P81022;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-OCT-2000 (Rel. 40, Last annotation update)
DE   UROTENSIN II (U-II) (UII).
OS   Polyodon spathula (North American paddlefish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Chondrostei; Acipenseriformes; Polyodontidae;
OC   Polyodon.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=SPINAL CORD;
RX   MEDLINE=96051494; PubMed=8536944;
RA   Waugh D., Youson J., Mims S.D., Sower S., Conlon J.M.;
RT   "Urotensin II from the river lamprey (Lampetra fluviatilis), the sea
RT   lamprey (Petromyzon marinus), and the paddlefish (Polyodon
RT   spathula).";
RL   Gen. Comp. Endocrinol. 99:323-332(1995).
CC   -!- FUNCTION: HAS A SUGGESTED ROLE IN OSMOREGULATION AND AS A
CC       CORTICOTROPIN-RELEASING FACTOR. PROBABLY INVOLVED IN SMOOTH
CC       MUSCLE STIMULATION.
CC   -!- SIMILARITY: BELONGS TO THE UROTENSIN 2 FAMILY.
DR   INTERPRO; IPR001483; -.
DR   PFAM; PF02083; Urotensin_II; 1.
DR   PROSITE; PS00984; UROTENSIN_II; 1.
KW   Hormone.
FT   DISULFID      6     11       BY SIMILARITY.
SQ   SEQUENCE   12 AA;  1410 MW;  7551E9DBB879CEBB CRC64;


  Query Match             24.1%;  Score 20;  DB 1;  Length 12;
  Best Local Similarity   75.0%;  Pred. No. 1e+03;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 TAEC 5
            |:||
Db       3 TSEC 6


RESULT   9
UN02_PINPS
ID   UN02_PINPS     STANDARD;      PRT;    13 AA.
AC   P81667;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
```

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DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   UNKNOWN PROTEIN FROM 2D-PAGE OF NEEDLES (N55) (FRAGMENTS).
OS   Pinus pinaster (Maritime pine).
OC   Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC   Coniferopsida; Coniferales; Pinaceae; Pinus.
RN   [1]
RP   SEQUENCE.
RC   TISSUE=NEEDLE;
RX   MEDLINE=99274088; PubMed=10344291;
RA   Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA   Frigerio J.-M., Plomion C.;
RT   "Separation and characterization of needle and xylem maritime pine
RT   proteins.";
RL   Electrophoresis 20:1098-1108(1999).
CC   -!- INDUCTION: BY WATER-STRESS.
CC   -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC       PROTEIN IS: 5.4, ITS MW IS: 43 KDA.
FT   NON_TER       1      1
FT   NON_CONS      7      8
FT   NON_TER      13     13
SQ   SEQUENCE   13 AA;  1559 MW;  966B5A43EF94B411 CRC64;
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```
  Query Match             24.1%;  Score 20;  DB 1;  Length 13;
  Best Local Similarity   66.7%;  Pred. No. 1.1e+03;
  Matches    4;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      10 TRGDVF 15
           || :||
Db       6 TRDNVF 11
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```
RESULT  10
RS11_SALTY
ID   RS11_SALTY     STANDARD;      PRT;     9 AA.
AC   O54296;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   01-OCT-2000 (Rel. 40, Last annotation update)
DE   30S RIBOSOMAL PROTEIN S11 (FRAGMENT).
GN   RPSK.
OS   Salmonella typhimurium.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Salmonella.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LT2;
RA   Bjorkman J., Hughes D., Andersson D.;
RL   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: S11 PLAYS AN ESSENTIAL ROLE FOR THE SELECTION OF THE
CC       CORRECT TRNA IN PROTEIN BIOSYNTHESIS. IT IS LOCATED ON THE LARGE
CC       LOBE OF THE SMALL SUBUNIT (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE S11P FAMILY OF RIBOSOMAL PROTEINS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AJ223236; CAA11202.1; -.
DR   STYGENE; SG10702; RPSK.
DR   INTERPRO; IPR001971; -.
DR   PROSITE; PS00054; RIBOSOMAL_S11; PARTIAL.
KW   Ribosomal protein.
FT   NON_TER       1      1
SQ   SEQUENCE   9 AA;  1139 MW;  7A5B140333277774 CRC64;
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  Query Match             22.9%;  Score 19;  DB 1;  Length 9;
  Best Local Similarity   42.9%;  Pred. No. 8.9e+04;
  Matches    3;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       5 CKPQVTR 11
           |:|   |
Db       1 CRPPKKR 7
```

```
RESULT  11
PEDI_HYDAT
ID   PEDI_HYDAT     STANDARD;      PRT;    13 AA.
AC   P80578;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   01-OCT-1996 (Rel. 34, Last annotation update)
DE   PEDIN.
OS   Hydra attenuata (Hydra) (Hydra vulgaris).
OC   Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
OC   Hydridae; Hydra.
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=96232307; PubMed=8674432;
RA   Hoffmeister S.A.H.;
RT   "Isolation and characterization of two new morphogenetically active
RT   peptides from Hydra vulgaris.";
RL   Development 122:1941-1948(1996).
CC   -!- FUNCTION: MORPHOGENETICALLY ACTIVE PEPTIDE. ACTIVE IN FOOT
CC       DEVELOPMENT.
KW   Morphogen.
SQ   SEQUENCE   13 AA;  1512 MW;  6F5266E3F37632CB CRC64;
```

```
  Query Match             22.9%;  Score 19;  DB 1;  Length 13;
  Best Local Similarity   50.0%;  Pred. No. 1.7e+03;
  Matches    3;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4 ECKPQV 9
           | :|:|
Db       2 ELRPEV 7
```

```
RESULT  12
OXYT_RAJCL
ID   OXYT_RAJCL     STANDARD;      PRT;     9 AA.
AC   P42994;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   01-NOV-1995 (Rel. 32, Last annotation update)
DE   GLUMITOCIN.
OS   Raja clavata (Thornback ray).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC   Elasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea;
OC   Rajiformes; Rajidae; Raja.
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=66123415; PubMed=5880565;
RA   Acher R., Chauvet J., Chauvet M.-T., Crepy D.;
RT   "Phylogeny of neurophyophyseal peptides: isolation of a new hormone,
RT   glumitocin (Ser 4-Gln 8-ocytocin) present in a cartilaginous fish,
RT   the ray (Raia clavata).";
RL   Biochim. Biophys. Acta 107:393-396(1965).
CC   -!- FUNCTION: ANTIDIURETIC HORMONE.
CC   -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR   INTERPRO; IPR000981; -.
DR   PFAM; PF00220; hormone4; 1.
DR   PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW   Hormone; Amidation.
FT   DISULFID      1      6
FT   MOD_RES       9      9       AMIDATION.
SQ   SEQUENCE   9 AA;  984 MW;  17E9C76EB455B04B CRC64;
```

```
  Query Match             21.1%;  Score 17.5;  DB 1;  Length 9;
  Best Local Similarity   50.0%;  Pred. No. 8.9e+04;
```

```
  Matches    4;  Conservative    1;  Mismatches    2;  Indels    1;  Gaps    1;

Qy      1 YTAECKPQ 8
          | : | ||
Db      2 YISNC-PQ 8


RESULT  13
BPP2_BOTJA
ID   BPP2_BOTJA     STANDARD;      PRT;    10 AA.
AC   P01022;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   01-FEB-1994 (Rel. 28, Last annotation update)
DE   BRADYKININ-POTENTIATING PEPTIDE 10B (ANGIOTENSIN-CONVERTING ENZYME
DE   INHIBITOR V-6-II).
OS   Bothrops jararaca (Jararaca).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Bothrops.
RN   [1]
RP   SEQUENCE.
RC   TISSUE=VENOM;
RX   MEDLINE=72118526; PubMed=4334402;
RA   Ondetti M.A., Williams N.J., Sabo E.F., Pluscec J., Weaver E.R.,
RA   Kocy O.;
RT   "Angiotensin-converting enzyme inhibitors from the venom of Bothrops
RT   jararaca. Isolation, elucidation of structure, and synthesis.";
RL   Biochemistry 10:4033-4039(1971).
CC   -!- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
CC       ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF
CC       BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
CC       IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
DR   PIR; A01255; XAVI6B.
KW   Hypotensive agent; Venom.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
SQ   SEQUENCE   10 AA;  1232 MW;  30C53546C7741773 CRC64;


  Query Match             20.5%;  Score 17;  DB 1;  Length 10;
  Best Local Similarity   50.0%;  Pred. No. 2.9e+03;
  Matches    2;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      6 KPQV 9
          :||:
Db      5 RPQI 8


RESULT  14
BPP3_BOTIN
ID   BPP3_BOTIN     STANDARD;      PRT;    11 AA.
AC   P30423;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   01-FEB-1994 (Rel. 28, Last annotation update)
DE   BRADYKININ-POTENTIATING PEPTIDE S4,3,2 (10C) (ANGIOTENSIN-CONVERTING
DE   ENZYME INHIBITOR).
OS   Bothrops insularis (Island jararaca) (Queimada jararaca).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Bothrops.
RN   [1]
RP   SEQUENCE.
RC   TISSUE=VENOM;
RX   MEDLINE=90351557; PubMed=2386615;
RA   Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT   "Primary structure and biological activity of bradykinin potentiating
RT   peptides from Bothrops insularis snake venom.";
RL   J. Protein Chem. 9:221-227(1990).
CC   -!- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
CC       ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF
CC       BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
CC       IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
DR   PIR; C37196; C37196.
KW   Hypotensive agent; Venom.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
SQ   SEQUENCE   11 AA;  1199 MW;  20B25813C7741777 CRC64;


  Query Match             20.5%;  Score 17;  DB 1;  Length 11;
  Best Local Similarity   50.0%;  Pred. No. 3.2e+03;
  Matches    2;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      6 KPQV 9
          :||:
Db      6 RPQI 9


RESULT  15
BPP4_BOTIN
ID   BPP4_BOTIN     STANDARD;      PRT;    11 AA.
AC   P30424;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   01-FEB-1994 (Rel. 28, Last annotation update)
DE   BRADYKININ-POTENTIATING PEPTIDE S4,1,2 (ANGIOTENSIN-CONVERTING
DE   ENZYME INHIBITOR).
OS   Bothrops insularis (Island jararaca) (Queimada jararaca).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Bothrops.
RN   [1]
RP   SEQUENCE.
RC   TISSUE=VENOM;
RX   MEDLINE=90351557; PubMed=2386615;
RA   Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT   "Primary structure and biological activity of bradykinin potentiating
RT   peptides from Bothrops insularis snake venom.";
RL   J. Protein Chem. 9:221-227(1990).
CC   -!- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
CC       ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF
CC       BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
CC       IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
DR   PIR; D37196; D37196.
KW   Hypotensive agent; Venom.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
SQ   SEQUENCE   11 AA;  1143 MW;  20BBBF13C7741777 CRC64;


  Query Match             20.5%;  Score 17;  DB 1;  Length 11;
  Best Local Similarity   50.0%;  Pred. No. 3.2e+03;
  Matches    2;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      6 KPQV 9
          :||:
Db      6 RPQI 9


Search completed: March  6, 2001, 09:50:33
Job time: 110 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: March 6, 2001, 09:48:28 ; Search time 19.79 Seconds
(without alignments)
88.839 Million cell updates/sec

Title: US-09-081-522-8
Perfect score: 83
Sequence: 1 YTAECKPQVTRGDVF 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 2289

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_15:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	33	39.8	11	9	Q38415	Q38415 bacteriopha
2	30	36.1	15	2	O69142	O69142 streptococc
3	25	30.1	10	6	Q9N1X1	Q9n1x1 equus cabal
4	24	28.9	11	2	Q48933	Q48933 mycobacteri
5	24	28.9	15	2	Q9X637	Q9x637 klebsiella
6	24	28.9	15	2	Q9X635	Q9x635 escherichia
7	22	26.5	15	11	Q9QV00	Q9qv00 rattus sp.
8	21	25.3	7	10	P82445	P82445 nicotiana t
9	21	25.3	11	7	O77871	O77871 oreochromis
10	21	25.3	11	7	O77872	O77872 oreochromis
11	21	25.3	11	7	O77873	O77873 oreochromis
12	21	25.3	12	4	Q9UC37	Q9uc37 homo sapien
13	21	25.3	13	2	P74844	P74844 salmonella
14	21	25.3	15	4	Q9Y4Z9	Q9y4z9 homo sapien
15	20	24.1	10	10	P82438	P82438 nicotiana t
16	20	24.1	14	10	P82322	P82322 pisum sativ
17	20	24.1	15	4	Q9UCY1	Q9ucy1 homo sapien
18	20	24.1	15	12	Q97092	Q97092 human immun
19	20	24.1	15	12	Q97094	Q97094 human immun
20	19	22.9	13	8	Q9T2U1	Q9t2u1 bos taurus
21	19	22.9	14	8	Q9MRF6	Q9mrf6 hordeum mur
22	19	22.9	14	12	Q89818	Q89818 murine minu
23	19	22.9	15	5	Q9TWD5	Q9twd5 locusta mig
24	19	22.9	15	8	Q9T355	Q9t355 synagrops b
25	19	22.9	15	13	Q9PRZ9	Q9prz9 micropogoni
26	18.5	22.3	15	5	Q9TXC8	Q9txc8 locusta mig
27	18	21.7	9	2	Q9R735	Q9r735 streptomyce
28	18	21.7	10	2	Q9ZIB1	Q9zib1 clostridium
29	18	21.7	12	4	Q9UMZ8	Q9umz8 homo sapien
30	18	21.7	12	10	Q41856	Q41856 zea mays (m
31	18	21.7	12	11	Q9QZY4	Q9qzy4 mus musculu
32	18	21.7	15	2	Q9R599	Q9r599 micrococcus
33	18	21.7	15	4	Q9UCC7	Q9ucc7 homo sapien
34	18	21.7	15	7	O19468	O19468 mus musculu
35	17	20.5	8	2	Q9S6D5	Q9s6d5 escherichia
36	17	20.5	9	4	Q16386	Q16386 homo sapien
37	17	20.5	9	4	Q99887	Q99887 homo sapien
38	17	20.5	11	7	O78119	O78119 oreochromis
39	17	20.5	11	13	Q90735	Q90735 gallus gall
40	17	20.5	13	2	Q9X9D7	Q9x9d7 bacillus ha
41	17	20.5	13	4	Q15537	Q15537 homo sapien
42	17	20.5	13	12	Q81769	Q81769 hepatitis c
43	17	20.5	13	12	Q81770	Q81770 hepatitis c
44	17	20.5	13	12	Q81781	Q81781 hepatitis c
45	17	20.5	13	12	Q81761	Q81761 hepatitis c

ALIGNMENTS

```
RESULT   1
Q38415
ID   Q38415      PRELIMINARY;      PRT;    11 AA.
AC   Q38415;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   ANT1 PROTEIN (FRAGMENT).
OS   Bacteriophage P7.
OC   Viruses; dsDNA viruses, no RNA stage; Tailed phages; Myoviridae.
OX   NCBI_TaxID=10682;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90335963; PubMed=1696181;
RA   Citron M., Schuster H.;
RT   "The c4 repressors of bacteriophages P1 and P7 are antisense RNAs.";
RL   Cell 62:591-598(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92319637; PubMed=1620606;
RA   Citron M., Schuster H.;
RT   "The c4 repressor of bacteriophage P1 is a processed 77 base antisense
RT   RNA.";
RL   Nucleic Acids Res. 20:3085-3090(1992).
DR   EMBL; M35139; AAA32437.1; -.
FT   NON_TER      11      11
SQ   SEQUENCE   11 AA;  1315 MW;  38A55C6D11B2C737 CRC64;


  Query Match             39.8%;  Score 33;  DB 9;  Length 11;
  Best Local Similarity   66.7%;  Pred. No. 15;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       6 KPQVTRGDV 14
           || ||| |:
Db       3 KPLVTRNDI 11


RESULT   2
O69142
ID   O69142      PRELIMINARY;      PRT;    15 AA.
AC   O69142;
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DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
DE   PROTEIN SIC (FRAGMENT).
GN   SIC.
OS   Streptococcus pyogenes.
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC   Streptococcus.
OX   NCBI_TaxID=1314;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=AP1;
RA   Berge A., Rasmussen M., Bjorck L.;
RL   Infect. Immun. 0:0-0(1998).
DR   EMBL; AF064540; AAC38769.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   15 AA;  1552 MW;  87655FEF847401FF CRC64;


  Query Match          36.1%;  Score 30;  DB 2;  Length 15;
  Best Local Similarity  83.3%;  Pred. No. 70;
  Matches    5;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       5 CKPQVT 10
           ||| ||
Db       3 CKPSVT 8


RESULT   3
Q9N1X1
ID   Q9N1X1      PRELIMINARY;      PRT;    10 AA.
AC   Q9N1X1;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   ALCOHOL DEHYDROGENASE 3 (FRAGMENT).
GN   ADH3.
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20082971; PubMed=10613847;
RA   Caetano A.R., Shiue Y.L., Lyons L.A., O'Brien S.J., Laughlin T.F.,
RA   Bowling A.T., Murray J.D.;
RT   "A comparative gene map of the horse (Equus caballus).";
RL   Genome Res. 9:1239-1249(1999).
DR   EMBL; AF134056; AAF31299.1; -.
FT   NON_TER       1      1
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1144 MW;  C4EA25676B02D6DD CRC64;


  Query Match          30.1%;  Score 25;  DB 6;  Length 10;
  Best Local Similarity  55.6%;  Pred. No. 3.7e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2 TAECKPQVT 10
           ||: :| ||
Db       2 TAQVEPWVT 10


RESULT   4
Q48933
ID   Q48933      PRELIMINARY;      PRT;    11 AA.
AC   Q48933; P77701; Q48932;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   ALKYL HYDROPEROXIDE REDUCTASE C (FRAGMENT).
GN   AHPC.
OS   Mycobacterium bovis.
OC   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC   Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX   NCBI_TaxID=1765;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC35728, AND ATCC35727;
RA   Zhang Y., Deretic V.;
RL   Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC35735;
RX   MEDLINE=96256622; PubMed=8655566;
RA   Dhandayuthapani S., Zhang Y., Deretic V.;
RT   "Oxidative stress response and its role in sensitivity to isoniazid in
RT   mycobacteria: characterization and inducibility of ahpC by peroxides
RT   in Mycobacterium smegmatis and lack of expression in M. aurum and M.
RT   tuberculosis.";
RL   J. Bacteriol. 178:3641-3649(1996).
DR   EMBL; U58031; AAB00320.1; -.
DR   EMBL; U57979; AAA99830.1; -.
DR   EMBL; U57978; AAA99829.1; -.
DR   EMBL; U57762; AAB00317.1; -.
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1231 MW;  455099E3A87041A7 CRC64;


  Query Match          28.9%;  Score 24;  DB 2;  Length 11;
  Best Local Similarity  55.6%;  Pred. No. 6.2e+02;
  Matches    5;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       7 PQVTRGDVF 15
           | :| || |
Db       2 PLLTIGDQF 10


RESULT   5
Q9X637
ID   Q9X637      PRELIMINARY;      PRT;    15 AA.
AC   Q9X637;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   MERT (FRAGMENT).
GN   MERT.
OS   Klebsiella oxytoca.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Klebsiella.
OX   NCBI_TaxID=571;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=509H;
RX   MEDLINE=97208220; PubMed=9055422;
RA   Liebert C.A., Wireman J., Smith T., Summers A.O.;
RT   "Phylogeny of mercury resistance (mer) operons of gram-negative
RT   bacteria isolated from the fecal flora of primates.";
RL   Appl. Environ. Microbiol. 63:1066-1076(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=509H;
RX   MEDLINE=98027386; PubMed=9361435;
RA   Wireman J., Liebert C.A., Smith T., Summers A.O.;
RT   "Association of mercury resistance with antibiotic resistance in the
RT   gram-negative fecal bacteria of primates.";
RL   Appl. Environ. Microbiol. 63:4494-4503(1997).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=509H;
RA   Wireman J., Liebert C.A., Smith T., Summers A.O.;
RT   "15-bp tandem repeats occur at a sharp transition in gc content in the
RT   mer operon.";
RL   Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF131272; AAD37141.1; -.
FT   NON_TER      15     15
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SQ   SEQUENCE   15 AA;  1492 MW;  65BFCFC9827A585D CRC64;


  Query Match             28.9%;  Score 24;  DB 2;  Length 15;
  Best Local Similarity   50.0%;  Pred. No. 8.5e+02;
  Matches    5;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      6 KPQVTRGDVF 15
          :||  || :|
Db      3 EPQNGRGALF 12


RESULT   6
Q9X635
ID   Q9X635      PRELIMINARY;      PRT;    15 AA.
AC   Q9X635;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   MERT (FRAGMENT).
GN   MERT.
OS   Escherichia coli.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Escherichia.
OX   NCBI_TaxID=562;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=390;
RX   MEDLINE=97208220; PubMed=9055422;
RA   Liebert C.A., Wireman J., Smith T., Summers A.O.;
RT   "Phylogeny of mercury resistance (mer) operons of gram-negative
RT   bacteria isolated from the fecal flora of primates.";
RL   Appl. Environ. Microbiol. 63:1066-1076(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=390;
RX   MEDLINE=98027386; PubMed=9361435;
RA   Wireman J., Liebert C.A., Smith T., Summers A.O.;
RT   "Association of mercury resistance with antibiotic resistance in the
RT   gram-negative fecal bacteria of primates.";
RL   Appl. Environ. Microbiol. 63:4494-4503(1997).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=390;
RA   Wireman J., Liebert C.A., Smith T., Summers A.O.;
RT   "15-bp tandem repeats occur at a sharp transition in gc content in the
RT   mer operon.";
RL   Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF131271; AAD37139.1; -.
FT   NON_TER      15     15
SQ   SEQUENCE   15 AA;  1492 MW;  65BFCFC9827A585D CRC64;


  Query Match             28.9%;  Score 24;  DB 2;  Length 15;
  Best Local Similarity   50.0%;  Pred. No. 8.5e+02;
  Matches    5;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      6 KPQVTRGDVF 15
          :||  || :|
Db      3 EPQNGRGALF 12


RESULT   7
Q9QV00
ID   Q9QV00      PRELIMINARY;      PRT;    15 AA.
AC   Q9QV00;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   EOSINOPHIL CATIONIC PROTEIN (FRAGMENT).
OS   Rattus sp.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10118;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=95375557; PubMed=7647580;
RA   Watanabe M., Nittoh T., Suzuki T., Kitoh A., Mue S., Ohuchi K.;
RT   "Isolation and partial characterization of eosinophil granule proteins
RT   in rats--eosinophil cationic protein and major basic protein.";
RL   Int. Arch. Allergy Immunol. 108:11-18(1995).
SQ   SEQUENCE   15 AA;  1785 MW;  2AF6D99C12EBD794 CRC64;


  Query Match             26.5%;  Score 22;  DB 11;  Length 15;
  Best Local Similarity   50.0%;  Pred. No. 2e+03;
  Matches    3;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 YTAECK 5
          :|  ||
Db      6 FTGHCK 11


RESULT   8
P82445
ID   P82445      PRELIMINARY;      PRT;     7 AA.
AC   P82445;
DT   01-JUN-2000 (TrEMBLrel. 14, Created)
DT   01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT   01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE   10 KDA CELL WALL PROTEIN (FRAGMENT).
OS   Nicotiana tabacum (Common tobacco).
OC   Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC   Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
OC   Solanales; Solanaceae; Nicotiana.
OX   NCBI_TaxID=4097;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=CV. PETIT HAVANA;
RA   Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA   Wojtaszek P., Bolwell G.P.;
RT   "Proteomic study of secondary cell wall proteins from transformed
RT   tobacco culture.";
RL   Planta 0:0-0(2000).
CC   -!- SUBCELLULAR LOCATION: CELL WALL.
CC   -!- TISSUE SPECIFICITY: XYLEM.
KW   Cell wall.
FT   NON_TER       7      7
SQ   SEQUENCE   7 AA;  758 MW;  69D2C1E862D1B2A0 CRC64;


  Query Match             25.3%;  Score 21;  DB 10;  Length 7;
  Best Local Similarity   71.4%;  Pred. No. 3.7e+05;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      9 VTRGDVF 15
          || | ||
Db      1 VTVGHVF 7


RESULT   9
O77871
ID   O77871      PRELIMINARY;      PRT;    11 AA.
AC   O77871;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   MHC CLASS II B LOCUS 1 (FRAGMENT).
OS   Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
OC   Cichlidae; Oreochromis.
OX   NCBI_TaxID=8128;
RN   [1]
RP   SEQUENCE FROM N.A.
```

```
RX   MEDLINE=98315113; PubMed=9649539;
RA   Malaga-Trillo E., McAndrew B., Vincek V., Zaleska-Rutczynska Z.,
RA   Sueltmann H., Figueroa F., Klein J.;
RT   "Linkage relationships and haplotype polymorphism among cichlid Mhc
RT   class II B loci.";
RL   Genetics 149:1527-1547(1998).
DR   EMBL; AF049980; AAC41319.1; -.
KW   MHC.
FT   NON_TER       1      1
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1133 MW;  283248EC3EB72728 CRC64;


  Query Match             25.3%;  Score 21;  DB 7;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 CKP 7
          |||
Db      7 CKP 9


RESULT  10
O77872
ID   O77872      PRELIMINARY;      PRT;    11 AA.
AC   O77872;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   MHC CLASS II B LOCUS 1 (FRAGMENT).
OS   Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
OC   Cichlidae; Oreochromis.
OX   NCBI_TaxID=8128;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98315113; PubMed=9649539;
RA   Malaga-Trillo E., McAndrew B., Vincek V., Zaleska-Rutczynska Z.,
RA   Sueltmann H., Figueroa F., Klein J.;
RT   "Linkage relationships and haplotype polymorphism among cichlid Mhc
RT   class II B loci.";
RL   Genetics 149:1527-1547(1998).
DR   EMBL; AF049981; AAC41320.1; -.
KW   MHC.
FT   NON_TER       1      1
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1133 MW;  283248EC3EB72728 CRC64;


  Query Match             25.3%;  Score 21;  DB 7;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 CKP 7
          |||
Db      7 CKP 9


RESULT  11
O77873
ID   O77873      PRELIMINARY;      PRT;    11 AA.
AC   O77873;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   MHC CLASS II B LOCUS 1 (FRAGMENT).
OS   Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
OC   Cichlidae; Oreochromis.
OX   NCBI_TaxID=8128;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98315113; PubMed=9649539;
RA   Malaga-Trillo E., McAndrew B., Vincek V., Zaleska-Rutczynska Z.,
RA   Sueltmann H., Figueroa F., Klein J.;
RT   "Linkage relationships and haplotype polymorphism among cichlid Mhc
RT   class II B loci.";
RL   Genetics 149:1527-1547(1998).
DR   EMBL; AF049982; AAC41321.1; -.
KW   MHC.
FT   NON_TER       1      1
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1133 MW;  283248EC3EB72728 CRC64;


  Query Match             25.3%;  Score 21;  DB 7;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 CKP 7
          |||
Db      7 CKP 9


RESULT  12
Q9UC37
ID   Q9UC37      PRELIMINARY;      PRT;    12 AA.
AC   Q9UC37;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   ALPHA B CRYSTALLIN FRAGMENT 5.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=92218434; PubMed=1560006;
RA   Kato K., Shinohara H., Goto S., Inaguma Y., Morishita R., Asano T.;
RT   "Copurification of small heat shock protein with alpha B crystallin
RT   from human skeletal muscle.";
RL   J. Biol. Chem. 267:7718-7725(1992).
SQ   SEQUENCE   12 AA;  1268 MW;  D37BD529CCC1B2CD CRC64;


  Query Match             25.3%;  Score 21;  DB 4;  Length 12;
  Best Local Similarity   71.4%;  Pred. No. 2.4e+03;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      4 ECKPQVT 10
          | || ||
Db      1 EEKPAVT 7


RESULT  13
P74844
ID   P74844      PRELIMINARY;      PRT;    13 AA.
AC   P74844;
DT   01-FEB-1997 (TrEMBLrel. 02, Created)
DT   01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   SIGMA FACTOR (FRAGMENT).
GN   FLIA.
OS   Salmonella typhimurium.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Salmonella.
OX   NCBI_TaxID=602;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=168-94;
RX   MEDLINE=97311993; PubMed=9168604;
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RA   Burnens A.P., Stanley J., Sack R., Hunziker P., Brodard I.,
RA   Nicolet J.;
RT   "The flagellin N-methylase gene fliB and an adjacent serovar-specific
RT   IS200 element in Salmonella typhimurium.";
RL   Microbiology 143:1539-1547(1997).
DR   EMBL; Z67749; CAA91563.1; -.
FT   NON_TER      13      13
SQ   SEQUENCE   13 AA;  1459 MW;  99199C0161421DC1 CRC64;


  Query Match             25.3%;  Score 21;  DB 2;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 YTAE 4
          ||||
Db      5 YTAE 8


RESULT  14
Q9Y4Z9
ID   Q9Y4Z9      PRELIMINARY;      PRT;    15 AA.
AC   Q9Y4Z9;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   FANCA PROTEIN (FRAGMENT).
GN   FANCA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   D'Apolito M., Ianzano L., Savino M., Rommens J., Zelante L.,
RA   Savoia A.;
RT   "Differential expression of FANCA and FANCC genes in human tissues and
RT   alternative splicing of FANCA transcripts.";
RL   Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ131189; CAB46099.1; -.
FT   NON_TER       1       1
SQ   SEQUENCE   15 AA;  1590 MW;  8732D75A24DCA4F0 CRC64;


  Query Match             25.3%;  Score 21;  DB 4;  Length 15;
  Best Local Similarity   50.0%;  Pred. No. 3e+03;
  Matches    4;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      5 CKPQVTRG 12
          | |   ||
Db      8 CGPSHLRG 15


RESULT  15
P82438
ID   P82438      PRELIMINARY;      PRT;    10 AA.
AC   P82438;
DT   01-JUN-2000 (TrEMBLrel. 14, Created)
DT   01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT   01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE   50 KDA CELL WALL PROTEIN (FRAGMENT).
OS   Nicotiana tabacum (Common tobacco).
OC   Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC   Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
OC   Solanales; Solanaceae; Nicotiana.
OX   NCBI_TaxID=4097;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=CV. PETIT HAVANA;
RA   Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA   Wojtaszek P., Bolwell G.P.;
RT   "Proteomic study of secondary cell wall proteins from transformed
RT   tobacco culture.";
RL   Planta 0:0-0(2000).
CC   -!- SUBCELLULAR LOCATION: CELL WALL.
CC   -!- TISSUE SPECIFICITY: XYLEM.
KW   Cell wall.
FT   NON_TER      10      10
SQ   SEQUENCE   10 AA;  1126 MW;  C68E32486AF77B46 CRC64;


  Query Match             24.1%;  Score 20;  DB 10;  Length 10;
  Best Local Similarity   50.0%;  Pred. No. 3e+03;
  Matches    4;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      7 PQVTRGDV 14
          ||   |:|
Db      2 PQYPXGNV 9


Search completed: March  6, 2001, 09:50:22
Job time: 114 sec
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